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 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Kljavin, Ivar J.
 Napier, Mary A.
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 Ile Ala Gly Phe Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu
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 Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His
 35 40 45
 Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
 50 55 60
 Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr
 65 70 75
 Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
 80 85 90
 Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
 95 100 105
 Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
 110 115 120
 Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
 125 130 135
 Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
 140 145 150

Arg Ile Ile Gln Glu Arg Asn Gly Val Leu Pro Asp Cys Leu Thr
 155 160
 Asp Gly Ser Asp Val Val Ser Asp Leu Glu His Glu Glu Met Lys
 170 175 180
 Ile Leu Arg Glu Val Leu Arg Lys Ser Lys Glu Glu Tyr Asp Gln
 185 190 195
 Glu Glu Glu Arg Lys Arg Lys Lys Gln Leu Ser Glu Ala Lys Thr
 200 205 210
 Glu Glu Pro Thr Val His Ser Ser Glu Ala Ala Ile Met Asn Asn
 215 220 225
 Ser Gln Gly Asp Gly Glu His Phe Ala His Pro Pro Ser Glu Val
 230 235 240
 Lys Met His Phe Ala Asn Gln Ser Ile Glu Pro Leu Gly Arg Lys
 245 250 255
 Val Glu Arg Ser Glu Thr Ser Ser Leu Pro Gln Lys Gly Leu Lys
 260 265 270
 Ile Pro Gly Leu Glu His Ala Ser Ile Glu Gly Pro Ile Ala Asn
 275 280 285
 Leu Ser Val Leu Gly Thr Glu Glu Leu Arg Gln Arg Glu His Tyr
 290 295 300
 Leu Lys Gln Lys Arg Asp Lys Leu Met Ser Met Arg Lys Asp Met
 305 310 315
 Arg Thr Lys Gln Ile Gln Asn Met Glu Gln Lys Gly Lys Pro Thr
 320 325 330
 Gly Glu Val Glu Glu Met Thr Glu Lys Pro Glu Met Thr Ala Glu
 335 340 345
 Glu Lys Gln Thr Leu Leu Lys Arg Arg Leu Leu Ala Glu Lys Leu
 350 355 360
 Lys Glu Glu Val Ile Asn Lys
 365

<210> 9
 <211> 418
 <212> DNA
 <213> Homo sapiens

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 aagggtacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150
 tgcacttctc ctcttgcaaa gacccataca tcacaggcca tttttgcaac 200
 ctgtgttggc agcagaagat ttactatct ttaagcaat gatgtgccag 250
 aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350
 ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400
 gaggaatatg accaggaa 418

<210> 10
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 10
 ttgacctata cagagattca tc 22

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 11
 ctaagaactt ccctcaggat ttt 23

<210> 12
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 12
 atgaagatca atttcaagaa gcattgcactt ctctctctgc 40

<210> 13
 <211> 2886
 <212> DNA
 <213> Homo sapiens

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 cactagaagc tcttctgagg gaggtaatta aaaaacacgt gaatggaaaa 200
 acagtgcgtg agtcacacct taatatgctc cttgtcaaca atgtatacat 250
 tctctgctagg tgccatatcc attgctttta gctcaagtcg catcttacta 300
 gtgaagtatt ctgccaatga agaaaacaag tatgattato ttccaactac 350
 tgtgaatgtg tgctcagaac tggatgaagc agttttctgt gtgcttgtgt 400
 cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450

toctggaagg aattctctga ttctcatgaag tggctccattc ctgcctttct 500
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 tttgggatga tgtagtctgt gctaaatatt ttgctgaaga agcagtttct 2050

cagacacaac atctcagaat ttttaattttt agaaattcat gggaaattgg 2100
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 agctgtgact attgtatatc tttccaagag ttgaaatgct ggcttcagaa 2350
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 gaatattaat actctaaaaa tagaaagacc agtaatatat aagtcacttt 2500
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<210> 14

<211> 424

<212> PRT

<213> Homo sapiens

<400> 14

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Thr	Met	Tyr	Thr	Phe	Leu	Leu	Gly	Ala	Ile	Phe	Ile	Ala	Leu	Ser
				20					25				30	
Ser	Ser	Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn
				35					40				45	
Lys	Tyr	Asp	Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu
				50					55				60	
Val	Lys	Leu	Val	Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys
				65					70				75	
Lys	Asp	His	Gln	Ser	Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu
				80					85				90	
Phe	Ser	Asp	Phe	Met	Lys	Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe
				95					100				105	
Leu	Asp	Asn	Leu	Ile	Val	Phe	Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro
				110					115				120	

Ala Met Ala Val	Ile Phe Ser Asn Phe	Ser Ile Ile Thr Thr	Ala
125		130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg	Arg Leu Asn Trp Ile	Gln
140		145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu	Ser Ile Val Ala Leu	Thr
155		160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn	Leu Ala Gly Arg Gly	Phe
170		175	180
His His Asp Ala	Phe Phe Ser Pro Ser	Asn Ser Cys Leu Leu	Phe
185		190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn	Cys Thr Ala Lys Glu	Trp
200		205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr	Thr Ala Arg Val Phe	Ser
215		220	225
His Ile Arg Leu	Gly Met Gly His Val	Leu Ile Ile Val Gln	Cys
230		235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr	Asn Glu Lys Ile Leu	Lys
245		250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile	Phe Ile Gln Asn Ser	Lys
260		265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn	Gly Leu Thr Leu Gly	Leu
275		280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys	Asn Cys Gly Phe Phe	Tyr
290		295	300
Gly His Ser Ala	Phe Ser Val Ala Leu	Ile Phe Val Thr Ala	Phe
305		310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu	Lys Phe Leu Asp Asn	Met
320		325	330
Phe His Val Leu	Met Ala Gln Val Thr	Thr Val Ile Ile Thr	Thr
335		340	345
Val Ser Val Leu	Val Phe Asp Phe Arg	Pro Ser Leu Glu Phe	Phe
350		355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser	Ile Phe Ile Tyr Asn	Ala
365		370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala	Pro Arg Gln Glu Arg	Ile
380		385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu	Arg Ser Ser Gly Asp	Gly
395		400	405
Glu Glu Leu Glu	Arg Leu Thr Lys Pro	Lys Ser Asp Glu Ser	Asp
410		415	420
Glu Asp Thr Phe			

<210> 15
 <211> 755
 <212> DNA
 <213> Homo sapiens

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 tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgtttctc 200
 cactagaagc ttttctgagg gaggtaatta aaaaacagtg gaatggaaaa 250
 acagtgcgtg agtcatcctg taatatgctc cttgtcaaca atgtatacat 300
 tcctgctagg tgccatattc attgctttta gctcaagtcg catcttacta 350
 gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 400
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 cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 500
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 ttatttctgt gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600
 cagccatggc tgttatcttc tcaaatttta gcattataac aacagctctt 650
 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700
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 cttta 755

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 16
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<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 17
 tcagagaatt ccttcagga 20

<210> 18
 <211> 40
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgtgt agtcatcctg taatatgtc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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gcggcctcgc gggcagagga gcatcccgtc taccaggctc caagcggcgt 150
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gacccctcgg tgggcctctg catcagcaa tcccctgga cctgcctggg 500
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<210> 20

<211> 458

<212> FRT

<213> Homo sapiens

<400> 20

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Trp	Ala	Glu	Pro	Gly	Met	Pro	Ser	Gln	Thr	Pro	Trp	Trp	Ala	Ser	20	25	30	
Ala	Ser	Ala	Asn	Pro	Pro	Gly	Pro	Ala	Trp	Val	Ala	Leu	Cys	Pro	35	40	45	
Gly	Ser	Ser	Ser	Pro	Arg	Pro	Trp	Pro	Ser	Leu	Pro	Thr	Ser	Ser	50	55	60	
Ser	Gly	Ser	Cys	Pro	Thr	Ser	His	Thr	Ala	Arg	Pro	Ile	Gly	Thr	65	70	75	
Cys	Phe	Ser	Ile	Ala	Ser	Leu	Lys	Gln	Trp	Ser	Arg	Val	Ser	Met	80	85	90	
Phe	Pro	Thr	Arg	Leu	Ser	Pro	Cys	Ser	Ser	Ala	Thr	Glu	Gln	Thr	95	100	105	

Glu Arg Asp Ser	Ala Thr Ala Tyr Arg	Met Thr Val Glu Val Leu	110	115	120
Gly Thr Val Leu	Gly Thr Ala Ile Gln	Gly Gln Ile Val Gly Gln	125	130	135
Ala Asp Thr Pro	Cys Phe Gln Asp Phe	Asn Ser Ser Thr Val Ala	140	145	150
Ser Gln Ser Ala	Asn His Thr His Gly	Thr Thr Ser His Arg Glu	155	160	165
Thr Gln Lys Ala	Tyr Leu Leu Ala Ala	Gly Val Ile Val Cys Ile	170	175	180
Tyr Ile Ile Cys	Ala Val Ile Leu Ile	Leu Gly Val Arg Glu Gln	185	190	195
Arg Glu Pro Tyr	Glu Ala Gln Gln Ser	Glu Pro Ile Ala Tyr Phe	200	205	210
Arg Gly Leu Arg	Leu Val Met Ser His	Gly Pro Tyr Ile Lys Leu	215	220	225
Ile Thr Gly Phe	Leu Phe Thr Ser Leu	Ala Phe Met Leu Val Glu	230	235	240
Gly Asn Phe Val	Leu Phe Cys Thr Tyr	Thr Leu Gly Phe Arg Asn	245	250	255
Glu Phe Gln Asn	Leu Leu Leu Ala Ile	Met Leu Ser Ala Thr Leu	260	265	270
Thr Ile Pro Ile	Trp Gln Trp Phe Leu	Thr Arg Phe Gly Lys Lys	275	280	285
Thr Ala Val Tyr	Val Gly Ile Ser Ser	Ala Val Pro Phe Leu Ile	290	295	300
Leu Val Ala Leu	Met Glu Ser Asn Leu	Ile Ile Thr Tyr Ala Val	305	310	315
Ala Val Ala Ala	Gly Ile Ser Val Ala	Ala Ala Phe Leu Leu Pro	320	325	330
Trp Ser Met Leu	Pro Asp Val Ile Asp	Asp Phe His Leu Lys Gln	335	340	345
Pro His Phe His	Gly Thr Glu Pro Ile	Phe Phe Ser Phe Tyr Val	350	355	360
Phe Phe Thr Lys	Phe Ala Ser Gly Val	Ser Leu Gly Ile Ser Thr	365	370	375
Leu Ser Leu Asp	Phe Ala Gly Tyr Gln	Thr Arg Gly Cys Ser Gln	380	385	390
Pro Glu Arg Val	Lys Phe Thr Leu Asn	Met Leu Val Thr Met Ala	395	400	405
Pro Ile Val Leu	Ile Leu Leu Gly Leu	Leu Leu Phe Lys Met Tyr	410	415	420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
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 440 445 450
 Ser Thr Glu Leu Ala Ser Ile Leu
 455

<210> 21
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 21
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 cggtttgga agaagacagc tgtatatgtt gggtatctcat cagcagtgcc 400
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 tgggtccatgc tgccctgatgt cattgacgac ttccatctga agcagcccca 550
 ctcccatgga accgagccca t 571

<210> 22
 <211> 1173
 <212> DNA
 <213> Homo sapiens

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 aaacagaaaa cctgttagaa atgtgtgtgt ttccagcaagg cctcagtttc 150
 cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200
 cattactgca gtaacactcc accatataga cccggcttta ccttatatca 250
 gtgacactgg tacagtagct ccagaaaaat gcttattttg ggcaatgtca 300
 aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350
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 ctggccttgt acttgggaata ctgagttgtt taggactttc tattgtggca 450

aacttcacaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500
 taccttttggat atgggctcat tatatatgtt tgttcagacc atcctttect 550
 accaaatgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600
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<210> 23
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 23
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 20 25 30
 Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp
 35 40 45
 Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu
 50 55 60
 Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
 65 70 75
 Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
 80 85 90
 Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
 95 100 105
 Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
 110 115 120
 His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr
 125 130 135

Met Phe Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile
140 145 150
His Gly Lys Gln Val Phe Trp Ile Arg Leu Leu Val Ile Trp
155 160 165
Cys Gly Val Ser Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu
170 175 180
His Ser Gly Asn Phe Gly Thr Asp Leu Glu Gln Lys Leu His Trp
185 190 195
Asn Pro Glu Asp Lys Gly Tyr Val Leu His Met Ile Thr Thr Ala
200 205 210
Ala Glu Trp Ser Met Ser Phe Ser Phe Phe Gly Phe Phe Leu Thr
215 220 225
Tyr Ile Arg Asp Phe Gln Lys Ile Ser Leu Arg Val Glu Ala Asn
230 235 240
Leu His Gly Leu Thr Leu Tyr Asp Thr Ala Pro Cys Pro Ile Asn
245 250 255
Asn Glu Arg Thr Arg Leu Leu Ser Arg Asp Ile
260 265

<210> 24
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 14, 484
<223> unknown base

<400> 24
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gagcggagat cctcaaacg cctagtgtt cgcgttccg gagaaaaatca 150
gcggtctaata taattcctct ggtttgtga agcagttacc aagaatcttc 200
aaccttttcc cacaaaagct aattgagtac acgttctctg tgagtacacg 250
ttcctgttga ttacaaaag gtgcaggtat gacaggtct gaagactaac 300
atattgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtggtttca 350
gcaaggctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400
ctttcatatt ttcatacat actgcagtaa cactccacca tatagaccg 450
gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 25
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 <210> 26
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 26
 ggagatagct gctatgggtt cttcaggcac aacttaacat gggaga 46
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 <211> 1399
 <212> DNA
 <213> Homo sapiens
 <400> 27
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 ccttctgtgc ttgcgcggct gcaccttcgc cttgtacttg ctgtcgacgc 150
 gactgccccg cgggcggaga ctgggctcca ccgaggagcg tggaggcagg 200
 tcgtgtgtgt tccctccga cctggcagag ctgcgggagc tctctgaggt 250
 ccttcgagag taccggaag agcaccaggc ctactgttgc ctgctcttct 300
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 agaaaatgct gtttgtggcc gggcgcggtg gctcacgcct gtaatccag 1150
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 agcctggcca agatggtgaa atcctgtctc taataaaaaa acaaaaatta 1250
 gccaggcggtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300
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 cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg
 20 25 30
 Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro
 35 40 45
 Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu
 50 55 60
 Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly
 65 70 75
 Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe
 80 85 90
 Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu
 95 100 105
 Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr
 110 115 120
 Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe
 125 130 135
 Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg
 140 145 150
 Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met
 155 160 165
 Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile
 170 175 180
 Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro
 185 190 195
 Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu
 200 205 210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu
 215 220
 Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys
 230 235 240
 Lys Phe Ser Gln Lys His Leu Gln Leu Asn Glu Thr Ser Thr Ala
 245 250 255
 Asn His Ile His Ser Arg Lys Asp Thr
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<210> 29
 <211> 1292
 <212> DNA
 <213> Homo sapiens

<400> 29
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 ggtttccgaa ctgccagctc agaataggaa aataactttg gattttatat 150
 tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaaactt 200
 tcagagactg ttgatttggg gagacagacc ggccatcagt gtggcatgctc 250
 agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300
 ctccagagacc ccccccgag tatcctctcc ttatagttgt gtataaggtt 350
 ctgcgaacct tgggattaat ctgtctcact gctactttg tgattcaacc 400
 tttcagccca ttagcacctg agccagtgt ttctggagct cacacctggc 450
 gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500
 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550
 accctttcca gactttgacc cctggtggac aaacgactgt gagcagaatg 600
 agtcagagcc cattctgccc aactgcactg gctgtgcccc gaaacacctg 650
 aaggtgatgc tcttggaaga cgcgccaaag aaatttgaga ggctccatcc 700
 actggtgatc aagacgggaa agcccctgtt ggaggaagag attcagcatt 750
 ttttgtgcca gtaccctgag ggcacagaag gcttctctga agggtttttc 800
 gccaaagtgt ggcgtgctt tcttgagcgg tgggttccat ttcttatcc 850
 atggaggaga cctctgaaca gatcacaat gttacgtgag ctttttctctg 900
 ttttcaactc cctgccattt ccaaaagatg cctctttaaa caagtgtctc 950
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 cctattttatc attggcagcg gtgaggccat gttgcagctc atccctccct 1050
 tccagtgcgg aagacattgt cagtctgtgg ccatgccaat agagccaggg 1100
 gatatcggtc atgtcgacac caccactgg aggtctctac ttatagccag 1150

aggggtccag cctttggtca tctgcgatgg aaccgcttcc tcagaactgt 1200
 aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccaggtt 1250
 gaaaggggaa aaataaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30

<211> 347

<212> FRT

<213> Homo sapiens

<400> 30

Met	Asp	Leu	Ala	Ala	Asn	Glu	Ile	Ser	Ile	Tyr	Asp	Lys	Leu	Ser	1	5	10	15
Glu	Thr	Val	Asp	Leu	Val	Arg	Gln	Thr	Gly	His	Gln	Cys	Gly	Met	20	25	30	
Ser	Glu	Lys	Ala	Ile	Glu	Lys	Phe	Ile	Arg	Gln	Leu	Leu	Glu	Lys	35	40	45	
Asn	Glu	Pro	Gln	Arg	Pro	Pro	Pro	Gln	Tyr	Pro	Leu	Leu	Ile	Val	50	55	60	
Val	Tyr	Lys	Val	Leu	Ala	Thr	Leu	Gly	Leu	Ile	Leu	Leu	Thr	Ala	65	70	75	
Tyr	Phe	Val	Ile	Gln	Pro	Phe	Ser	Pro	Leu	Ala	Pro	Glu	Pro	Val	80	85	90	
Leu	Ser	Gly	Ala	His	Thr	Trp	Arg	Ser	Leu	Ile	His	His	Ile	Arg	95	100	105	
Leu	Met	Ser	Leu	Pro	Ile	Ala	Lys	Lys	Tyr	Met	Ser	Glu	Asn	Lys	110	115	120	
Gly	Val	Pro	Leu	His	Gly	Gly	Asp	Glu	Asp	Arg	Pro	Phe	Pro	Asp	125	130	135	
Phe	Asp	Pro	Trp	Trp	Thr	Asn	Asp	Cys	Glu	Gln	Asn	Glu	Ser	Glu	140	145	150	
Pro	Ile	Pro	Ala	Asn	Cys	Thr	Gly	Cys	Ala	Gln	Lys	His	Leu	Lys	155	160	165	
Val	Met	Leu	Leu	Glu	Asp	Ala	Pro	Arg	Lys	Phe	Glu	Arg	Leu	His	170	175	180	
Pro	Leu	Val	Ile	Lys	Thr	Gly	Lys	Pro	Leu	Leu	Glu	Glu	Glu	Ile	185	190	195	
Gln	His	Phe	Leu	Cys	Gln	Tyr	Pro	Glu	Ala	Thr	Glu	Gly	Phe	Ser	200	205	210	
Glu	Gly	Phe	Phe	Ala	Lys	Trp	Trp	Arg	Cys	Phe	Pro	Glu	Arg	Trp	215	220	225	
Phe	Pro	Phe	Pro	Tyr	Pro	Trp	Arg	Arg	Pro	Leu	Asn	Arg	Ser	Gln	230	235	240	
Met	Leu	Arg	Glu	Leu	Phe	Pro	Val	Phe	Thr	His	Leu	Pro	Phe	Pro	245	250	255	

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<210> 33

<211> 1003

<212> PRT

<213> Homo sapiens

<400> 33

Met	Ser	Gln	Phe	Glu	Met	Asp	Thr	Tyr	Ala	Lys	Ser	His	Asp	Leu
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Met	Ser	Gly	Phe	Trp	Asn	Ala	Cys	Tyr	Asp	Met	Leu	Met	Ser	Ser
				20					25					30

Gly	Gln	Arg	Arg	Gln	Trp	Glu	Arg	Ala	Gln	Ser	Arg	Arg	Ala	Phe
				35					40					45

Gln	Glu	Leu	Val	Leu	Glu	Pro	Ala	Gln	Arg	Arg	Ala	Arg	Leu	Glu
				50					55					60

Gly	Leu	Arg	Tyr	Thr	Ala	Val	Leu	Lys	Gln	Gln	Ala	Thr	Gln	His
				65					70					75

Ser	Met	Ala	Leu	Leu	His	Trp	Gly	Ala	Leu	Trp	Arg	Gln	Leu	Ala
				80					85					90

Ser	Pro	Cys	Gly	Ala	Trp	Ala	Leu	Arg	Asp	Thr	Pro	Ile	Pro	Arg
				95					100					105

Trp	Lys	Leu	Ser	Ser	Ala	Glu	Thr	Tyr	Ser	Arg	Met	Arg	Leu	Lys
				110					115					120

Leu	Val	Pro	Asn	His	His	Phe	Asp	Pro	His	Leu	Glu	Ala	Ser	Ala
				125					130					135

Leu	Arg	Asp	Asn	Leu	Gly	Glu	Val	Pro	Leu	Thr	Pro	Thr	Glu	Glu
				140					145					150

Ala	Ser	Leu	Pro	Leu	Ala	Val	Thr	Lys	Glu	Ala	Lys	Val	Ser	Thr
				155					160					165

Pro	Pro	Glu	Leu	Leu	Gln	Glu	Asp	Gln	Leu	Gly	Glu	Asp	Glu	Leu
				170					175					180

Ala	Glu	Leu	Glu	Thr	Pro	Met	Glu	Ala	Ala	Glu	Leu	Asp	Glu	Gln
				185					190					195

Arg	Glu	Lys	Leu	Val	Leu	Ser	Ala	Glu	Cys	Gln	Leu	Val	Thr	Val
				200					205					210

Val	Ala	Val	Val	Pro	Gly	Leu	Leu	Glu	Val	Thr	Thr	Gln	Asn	Val
				215					220					225

Tyr	Phe	Tyr	Asp	Gly	Ser	Thr	Glu	Arg	Val	Glu	Thr	Glu	Glu	Gly
				230					235					240

Ile	Gly	Tyr	Asp	Phe	Arg	Arg	Pro	Leu	Ala	Gln	Leu	Arg	Glu	Val
				245					250					255

His	Leu	Arg	Arg	Phe	Asn	Leu	Arg	Arg	Ser	Ala	Leu	Glu	Leu	Phe
				260					265					270

Phe	Ile	Asp	Gln	Ala 275	Asn	Tyr	Phe	Leu	Asn 280	Phe	Pro	Cys	Lys	Val 285
Gly	Thr	Thr	Pro	Val 290	Ser	Ser	Pro	Ser	Gln 295	Thr	Pro	Arg	Pro	Gln 300
Pro	Gly	Pro	Ile	Pro 305	Pro	His	Thr	Gln	Val 310	Arg	Asn	Gln	Val	Tyr 315
Ser	Trp	Leu	Leu	Arg 320	Leu	Arg	Pro	Pro	Ser 325	Gln	Gly	Tyr	Leu	Ser 330
Ser	Arg	Ser	Pro	Gln 335	Glu	Met	Leu	Arg	Ala 340	Ser	Gly	Leu	Thr	Gln 345
Lys	Trp	Val	Gln	Arg 350	Glu	Ile	Ser	Asn	Phe 355	Glu	Tyr	Leu	Met	Gln 360
Leu	Asn	Thr	Ile	Ala 365	Gly	Arg	Thr	Tyr	Asn 370	Asp	Leu	Ser	Gln	Tyr 375
Pro	Val	Phe	Pro	Trp 380	Val	Leu	Gln	Asp	Tyr 385	Val	Ser	Pro	Thr	Leu 390
Asp	Leu	Ser	Asn	Pro 395	Ala	Val	Phe	Arg	Asp 400	Leu	Ser	Lys	Pro	Ile 405
Gly	Val	Val	Asn	Pro 410	Lys	His	Ala	Gln	Leu 415	Val	Arg	Glu	Lys	Tyr 420
Glu	Ser	Phe	Glu	Asp 425	Pro	Ala	Gly	Thr	Ile 430	Asp	Lys	Phe	His	Tyr 435
Gly	Thr	His	Tyr	Ser 440	Asn	Ala	Ala	Gly	Val 445	Met	His	Tyr	Leu	Ile 450
Arg	Val	Glu	Pro	Phe 455	Thr	Ser	Leu	His	Val 460	Gln	Leu	Gln	Ser	Gly 465
Arg	Phe	Asp	Cys	Ser 470	Asp	Arg	Gln	Phe	His 475	Ser	Val	Ala	Ala	Ala 480
Trp	Gln	Ala	Arg	Leu 485	Glu	Ser	Pro	Ala	Asp 490	Val	Lys	Glu	Leu	Ile 495
Pro	Glu	Phe	Phe	Tyr 500	Phe	Pro	Asp	Phe	Leu 505	Glu	Asn	Gln	Asn	Gly 510
Phe	Asp	Leu	Gly	Cys 515	Leu	Gln	Leu	Thr	Asn 520	Glu	Lys	Val	Gly	Asp 525
Val	Val	Leu	Pro	Pro 530	Trp	Ala	Ser	Ser	Pro 535	Glu	Asp	Phe	Ile	Gln 540
Gln	His	Arg	Gln	Ala 545	Leu	Glu	Ser	Glu	Tyr 550	Val	Ser	Ala	His	Leu 555
His	Glu	Trp	Ile	Asp 560	Leu	Ile	Phe	Gly	Tyr 565	Lys	Gln	Arg	Gly	Pro 570
Ala	Ala	Glu	Glu	Ala 575	Leu	Asn	Val	Phe	Tyr 580	Tyr	Cys	Thr	Tyr	Glu 585

Gly	Ala	Val	Asp	Leu 590	Asp	His	Val	Thr	Asp 595	Glu	Arg	Glu	Arg	Lys 600
Ala	Leu	Glu	Gly	Ile 605	Ile	Ser	Asn	Phe	Gly 610	Gln	Thr	Pro	Cys	Gln 615
Leu	Leu	Lys	Glu	Pro 620	His	Pro	Thr	Arg	Leu 625	Ser	Ala	Glu	Glu	Ala 630
Ala	His	Arg	Leu	Ala 635	Arg	Leu	Asp	Thr	Asn 640	Ser	Pro	Ser	Ile	Phe 645
Gln	His	Leu	Asp	Glu 650	Leu	Lys	Ala	Phe	Phe 655	Ala	Glu	Val	Thr	Val 660
Ser	Ala	Ser	Gly	Leu 665	Leu	Gly	Thr	His	Ser 670	Trp	Leu	Pro	Tyr	Asp 675
Arg	Asn	Ile	Ser	Asn 680	Tyr	Phe	Ser	Phe	Ser 685	Lys	Asp	Pro	Thr	Met 690
Gly	Ser	His	Lys	Thr 695	Gln	Arg	Leu	Leu	Ser 700	Gly	Pro	Trp	Val	Pro 705
Gly	Ser	Gly	Val	Ser 710	Gly	Gln	Ala	Leu	Ala 715	Val	Ala	Pro	Asp	Gly 720
Lys	Leu	Leu	Phe	Ser 725	Gly	Gly	His	Trp	Asp 730	Gly	Ser	Leu	Arg	Val 735
Thr	Ala	Leu	Pro	Arg 740	Gly	Lys	Leu	Leu	Ser 745	Gln	Leu	Ser	Cys	His 750
Leu	Asp	Val	Val	Thr 755	Cys	Leu	Ala	Leu	Asp 760	Thr	Cys	Gly	Ile	Tyr 765
Leu	Ile	Ser	Gly	Ser 770	Arg	Asp	Thr	Thr	Cys 775	Met	Val	Trp	Arg	Leu 780
Leu	His	Gln	Gly	Gly 785	Leu	Ser	Val	Gly	Leu 790	Ala	Pro	Lys	Pro	Val 795
Gln	Val	Leu	Tyr	Gly 800	His	Gly	Ala	Ala	Val 805	Ser	Cys	Val	Ala	Ile 810
Ser	Thr	Glu	Leu	Asp 815	Met	Ala	Val	Ser	Gly 820	Ser	Glu	Asp	Gly	Thr 825
Val	Ile	Ile	His	Thr 830	Val	Arg	Arg	Gly	Gln 835	Phe	Val	Ala	Ala	Leu 840
Arg	Pro	Leu	Gly	Ala 845	Thr	Phe	Pro	Gly	Pro 850	Ile	Phe	His	Leu	Ala 855
Leu	Gly	Ser	Glu	Gly 860	Gln	Ile	Val	Val	Gln 865	Ser	Ser	Ala	Trp	Glu 870
Arg	Pro	Gly	Ala	Gln 875	Val	Thr	Tyr	Ser	Leu 880	His	Leu	Tyr	Ser	Val 885
Asn	Gly	Lys	Leu	Arg 890	Ala	Ser	Leu	Pro	Leu 895	Ala	Glu	Gln	Pro	Thr 900

Ala	Leu	Thr	Val	Thr	Glu	Asp	Phe	Val	Leu	Leu	Gly	Thr	Ala	Gln
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Cys	Ala	Leu	His	Ile	Leu	Gln	Leu	Asn	Thr	Leu	Leu	Pro	Ala	Ala
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Pro	Pro	Leu	Pro	Met	Lys	Val	Ala	Ile	Arg	Ser	Val	Ala	Val	Thr
				935					940					945
Lys	Glu	Arg	Ser	His	Val	Leu	Val	Gly	Leu	Glu	Asp	Gly	Lys	Leu
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Ile	Val	Val	Val	Ala	Gly	Gln	Pro	Ser	Glu	Val	Arg	Ser	Ser	Gln
				965					970					975
Phe	Ala	Arg	Lys	Leu	Trp	Arg	Ser	Ser	Arg	Arg	Ile	Ser	Gln	Val
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<213> Artificial Sequence

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<210> 35

<211> 1395

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<213> Homo sapiens

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ttcaatctgc aaatctatgg ggtcctgggg ctctttctgga cccttaactg 200

ggtaactggcc ctggggccaat gcgtcctcgc tggaqccttt gcctccttct 250

actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct 300

gccttcattcc gcacactccg ttaccacact gggtcattgg catttggagc 350

cctcatcctg acccttggtgc agatagcccg ggtcatcttg gagtatatattg 400

accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc 450

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ccgcaatgca tacatcatga tcgccatcta cgggaagaat ttctgtgtct 550

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<213> Homo sapiens

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Leu	Ala	Gly	Ala	Phe	Ala	Ser	Phe	Tyr	Trp	Ala	Phe	His	Lys	Pro
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Gln	Asp	Ile	Pro	Thr	Phe	Pro	Leu	Ile	Ser	Ala	Phe	Ile	Arg	Thr
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Leu	Arg	Tyr	His	Thr	Gly	Ser	Leu	Ala	Phe	Gly	Ala	Leu	Ile	Leu
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Thr	Leu	Val	Gln	Ile	Ala	Arg	Val	Ile	Leu	Glu	Tyr	Ile	Asp	His
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Lys Leu Arg Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys
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Cys Phe Lys Cys Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe
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260 265 270

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Asn Lys Lys Arg Lys Lys
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<211> 22
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 37
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<212> DNA
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<400> 38
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<210> 39
<211> 50

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 35 40 45
 Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr
 50 55 60
 Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile
 65 70 75
 Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp
 80 85 90
 Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn
 95 100 105
 Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys
 110 115 120
 Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg
 125 130 135
 Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly
 140 145 150
 Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val
 155 160 165
 Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg
 170 175 180
 Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly
 185 190 195
 Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser
 200 205 210
 Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr
 215 220 225
 Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr
 230 235 240
 Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

245	250	255
Asn Glu Asp Glu	Glu Asn Thr Leu Ser	Val Asp Cys Thr Arg Ile
260	265	270
Ser Phe Glu Tyr	Asp Leu Arg Leu Val	Leu Tyr Gln His Trp Ser
275	280	285
Leu His Asp Ser	Leu Cys Asn Thr Ser	Tyr Thr Ala Ala Arg Phe
290	295	300
Lys Leu Trp Ser	Val His Gly Gln Lys	Arg Leu Gln Glu Phe Leu
305	310	315
Ala Asp Met Gly	Leu Pro Leu Lys Gln	Val Lys Gln Lys Phe Gln
320	325	330
Ala Met Asp Ile	Ser Leu Lys Glu Asn	Leu Arg Glu Met Ile Glu
335	340	345
Glu Ser Ala Asn	Lys Phe Gly Met Lys	Asp Met Arg Val Gln Thr
350	355	360
Phe Ser Ile His	Phe Gly Phe Lys His	Lys Phe Leu Ala Ser Asp
365	370	375
Val Val Phe Ala	Thr Met Ser Leu Met	Glu Ser Pro Glu Lys Asp
380	385	390
Gly Ser Gly Thr	Asp His Phe Ile Gln	Ala Leu Asp Ser Leu Ser
395	400	405
Arg Ser Asn Leu	Asp Lys Leu Tyr His	Gly Leu Glu Leu Ala Lys
410	415	420
Lys Gln Leu Arg	Ala Thr Gln Gln Thr	Ile Ala Ser Cys Leu Cys
425	430	435
Thr Asn Leu Val	Ile Ser Gln Gly Pro	Phe Leu Tyr Cys Ser Leu
440	445	450
Met Glu Gly Thr	Pro Asp Val Met Leu	Phe Ser Arg Pro Ala Ser
455	460	465
Leu Ser Leu Leu	Ser Lys His Leu Leu	Lys Ser Phe Val Cys Ser
470	475	480
Thr Lys Asn Arg	Arg Cys Lys Leu Leu	Pro Leu Val Met Ala Ala
485	490	495
Pro Leu Ser Met	Glu His Gly Thr Val	Thr Val Val Gly Ile Pro
500	505	510
Pro Glu Thr Asp	Ser Ser Asp Arg Lys	Asn Phe Phe Gly Arg Ala
515	520	525
Phe Glu Lys Ala	Ala Glu Ser Thr Ser	Ser Arg Met Leu His Asn
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Lys Phe Leu Asp	Ala Leu Ile Ser Leu	Leu Ser

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 <222> 44, 118, 172, 183
 <223> unknown base

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<210> 44
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<210> 45
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 35 40 45
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 50 55 60
 Pro His Ala Leu Pro Glu Ile Arg Pro Tyr Ile Asn Ile Thr Ile
 65 70 75
 Leu Lys Gly Asp Lys Gly Asp Pro Gly Pro Met Gly Leu Pro Gly
 80 85 90
 Tyr Met Gly Arg Glu Gly Pro Gln Gly Glu Pro Gly Pro Gln Gly
 95 100 105
 Ser Lys Gly Asp Lys Gly Glu Met Gly Ser Pro Gly Ala Pro Cys
 110 115 120
 Gln Lys Arg Phe Phe Ala Phe Ser Val Gly Arg Lys Thr Ala Leu
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 Ala Pro Leu Arg Gly Ile Tyr Phe Phe Ser Leu Asn Val His Ser
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 Trp Asn Tyr Lys Glu Thr Tyr Val His Ile Met His Asn Gln Lys
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 Glu Ala Val Ile Leu Tyr Ala Gln Pro Ser Glu Arg Ser Ile Met

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Val Ser Asn Leu	Ser Leu Gln Ala Leu	Pro Gly Asp Leu Ser	Gly
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 tcagtgaacc tcttgaatct gtttagtctc ctttttcaac aaaggagtgt 3200
 gttcagaaaa ggagagagag gctgagatca ttcaggagtt tgttgggcag 3250
 caagcatgga gcttcttgca caaattctgg gtccataaac aacccccaaa 3300

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<210> 62
 <211> 756
 <212> PRT
 <213> Homo sapiens

<400> 62
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 35 40 45
 Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro
 50 55 60
 Leu Pro Ala Gly Pro Gly Glu Glu Trp Glu Arg Arg Pro Gln Glu
 65 70 75
 Pro Arg Pro Pro Lys Arg Ala Thr Lys Pro Lys Lys Ala Pro Lys
 80 85 90
 Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Gly Lys His Ser
 95 100 105
 Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn
 110 115 120
 Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser
 125 130 135
 Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln
 140 145 150
 Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg
 155 160 165
 Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr
 170 175 180
 Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile

	185	190	195
Glu Val Asp Ala	Arg Arg Leu Thr Arg	Phe Thr Gly Val Ile	Thr
	200	205	210
Gln Gly Arg Asn	Ser Leu Trp Leu Ser	Asp Trp Val Thr Ser	Tyr
	215	220	225
Lys Val Met Val	Ser Asn Asp Ser His	Thr Trp Val Thr Val	Lys
	230	235	240
Asn Gly Ser Gly	Asp Met Ile Phe Glu	Gly Asn Ser Glu Lys	Glu
	245	250	255
Ile Pro Val Leu	Asn Glu Leu Pro Val	Pro Met Val Ala Arg	Tyr
	260	265	270
Ile Arg Ile Asn	Pro Gln Ser Trp Phe	Asp Asn Gly Ser Ile	Cys
	275	280	285
Met Arg Met Glu	Ile Leu Gly Cys Pro	Leu Pro Asp Pro Asn Asn	
	290	295	300
Tyr Tyr His Arg	Arg Asn Glu Met Thr	Thr Thr Asp Asp Leu Asp	
	305	310	315
Phe Lys His His	Asn Tyr Lys Glu Met	Arg Gln Leu Met Lys Val	
	320	325	330
Val Asn Glu Met	Cys Pro Asn Ile Thr	Arg Ile Tyr Asn Ile Gly	
	335	340	345
Lys Ser His Gln	Gly Leu Lys Leu Tyr	Ala Val Glu Ile Ser Asp	
	350	355	360
His Pro Gly Glu	His Glu Val Gly Glu	Pro Glu Phe His Tyr Ile	
	365	370	375
Ala Gly Ala His	Gly Asn Glu Val Leu	Gly Arg Glu Leu Leu Leu	
	380	385	390
Leu Leu Val Gln	Phe Val Cys Gln Glu	Tyr Leu Ala Arg Asn Ala	
	395	400	405
Arg Ile Val His	Leu Val Glu Glu Thr	Arg Ile His Val Leu Pro	
	410	415	420
Ser Leu Asn Pro	Asp Gly Tyr Glu Lys	Ala Tyr Glu Gly Gly Ser	
	425	430	435
Glu Leu Gly Gly	Trp Ser Leu Gly Arg	Trp Thr His Asp Gly Ile	
	440	445	450
Asp Ile Asn Asn	Asn Phe Pro Asp Leu	Asn Thr Leu Leu Trp Glu	
	455	460	465
Ala Glu Asp Arg	Gln Asn Val Pro Arg	Lys Val Pro Asn His Tyr	
	470	475	480
Ile Ala Ile Pro	Glu Trp Phe Leu Ser	Glu Asn Ala Thr Val Ala	
	485	490	495
Ala Glu Thr Arg	Ala Val Ile Ala Trp	Met Glu Lys Ile Pro Phe	

				500					505						510
Val	Leu	Gly	Gly	Asn 515	Leu	Gln	Gly	Gly	Glu 520	Leu	Val	Val	Ala	Tyr 525	
Pro	Tyr	Asp	Leu	Val 530	Arg	Ser	Pro	Trp	Lys 535	Thr	Gln	Glu	His	Thr 540	
Pro	Thr	Pro	Asp	Asp 545	His	Val	Phe	Arg	Trp 550	Leu	Ala	Tyr	Ser	Tyr 555	
Ala	Ser	Thr	His	Arg 560	Leu	Met	Thr	Asp	Ala 565	Arg	Arg	Arg	Val	Cys 570	
His	Thr	Glu	Asp	Phe 575	Gln	Lys	Glu	Glu	Gly 580	Thr	Val	Asn	Gly	Ala 585	
Ser	Trp	His	Thr	Val 590	Ala	Gly	Ser	Leu	Asn 595	Asp	Phe	Ser	Tyr	Leu 600	
His	Thr	Asn	Cys	Phe 605	Glu	Leu	Ser	Ile	Tyr 610	Val	Gly	Cys	Asp	Lys 615	
Tyr	Pro	His	Glu	Ser 620	Gln	Leu	Pro	Glu	Glu 625	Trp	Glu	Asn	Asn	Arg 630	
Glu	Ser	Leu	Ile	Val 635	Phe	Met	Glu	Gln	Val 640	His	Arg	Gly	Ile	Lys 645	
Gly	Leu	Val	Arg	Asp 650	Ser	His	Gly	Lys	Gly 655	Ile	Pro	Asn	Ala	Ile 660	
Ile	Ser	Val	Glu	Gly 665	Ile	Asn	His	Asp	Ile 670	Arg	Thr	Ala	Asn	Arg 675	
Gly	Asp	Tyr	Trp	Arg 680	Leu	Leu	Asn	Pro	Gly 685	Glu	Tyr	Val	Val	Thr 690	
Ala	Lys	Ala	Glu	Gly 695	Phe	Thr	Ala	Ser	Thr 700	Lys	Asn	Cys	Met	Val 705	
Gly	Tyr	Asp	Met	Gly 710	Ala	Thr	Arg	Cys	Asp 715	Phe	Thr	Leu	Ser	Lys 720	
Thr	Asn	Met	Ala	Arg 725	Ile	Arg	Glu	Ile	Met 730	Glu	Lys	Phe	Gly	Lys 735	
Gln	Pro	Val	Ser	Leu 740	Pro	Ala	Arg	Arg	Leu 745	Lys	Leu	Arg	Gly	Arg 750	
Lys	Arg	Arg	Gln	Arg 755	Gly										

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<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 63
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<210> 64
 <211> 24
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<220>
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<400> 64
 cgcgatgtag tggaactcgg gctc 24

<210> 65
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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 atccgcataa accctcagtc ctgggttgat aatggggagca tctgcatgag 50

<210> 66
 <211> 2854
 <212> DNA
 <213> Homo sapiens

<400> 66
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 gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250
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 ttgagaaaaga actttctaaa gtgagggaat atgtccaatt aattagtgtg 400
 tatgaaaaga aactgtttaa cctaactgtc cgaattgaca tcatggagaa 450
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 aaagatcaaa acaccccctg cgtccaccct cctcccactc cagggagctg 750
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 actggagagg gttttcttat ctatatggtg cttggggtag ggattactct 850
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aaaa 2854

<210> 67
<211> 510
<212> PRT
<213> Homo sapiens

<400> 67
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20 25 30
Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser
35 40 45
Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu
50 55 60
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly
65 70 75
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro
80 85 90
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
95 100 105
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val
110 115 120
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu
125 130 135
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser
140 145 150
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu
155 160 165
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser
170 175 180
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr
185 190 195
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu
200 205 210

Ala Ile Arg Arg	Glu Ile Val Ala Leu	Lys Thr Lys Leu Lys Glu
215		220 225
Cys Glu Ala Ser	Lys Asp Gln Asn Thr	Pro Val Val His Pro Pro
230		235 240
Pro Thr Pro Gly	Ser Cys Gly His Gly	Gly Val Val Asn Ile Ser
245		250 255
Lys Pro Ser Val	Val Gln Leu Asn Trp	Arg Gly Phe Ser Tyr Leu
260		265 270
Tyr Gly Ala Trp	Gly Arg Asp Tyr Ser	Pro Gln His Pro Asn Lys
275		280 285
Gly Leu Tyr Trp	Val Ala Pro Leu Asn	Thr Asp Gly Arg Leu Leu
290		295 300
Glu Tyr Tyr Arg	Leu Tyr Asn Thr Leu	Asp Asp Leu Leu Leu Tyr
305		310 315
Ile Asn Ala Arg	Glu Leu Arg Ile Thr	Tyr Gly Gln Gly Ser Gly
320		325 330
Thr Ala Val Tyr	Asn Asn Asn Met Tyr	Val Asn Met Tyr Asn Thr
335		340 345
Gly Asn Ile Ala	Arg Val Asn Leu Thr	Thr Asn Thr Ile Ala Val
350		355 360
Thr Gln Thr Leu	Pro Asn Ala Ala Tyr	Asn Asn Arg Phe Ser Tyr
365		370 375
Ala Asn Val Ala	Trp Gln Asp Ile Asp	Phe Ala Val Asp Glu Asn
380		385 390
Gly Leu Trp Val	Ile Tyr Ser Thr Glu	Ala Ser Thr Gly Asn Met
395		400 405
Val Ile Ser Lys	Leu Asn Asp Thr Thr	Leu Gln Val Leu Asn Thr
410		415 420
Trp Tyr Thr Lys	Gln Tyr Lys Pro Ser	Ala Ser Asn Ala Phe Met
425		430 435
Val Cys Gly Val	Leu Tyr Ala Thr Arg	Thr Met Asn Thr Arg Thr
440		445 450
Glu Glu Ile Phe	Tyr Tyr Tyr Asp Thr	Asn Thr Gly Lys Glu Gly
455		460 465
Lys Leu Asp Ile	Val Met His Lys Met	Gln Glu Lys Val Gln Ser
470		475 480
Ile Asn Tyr Asn	Pro Phe Asp Gln Lys	Leu Tyr Val Tyr Asn Asp
485		490 495
Gly Tyr Leu Leu	Asn Tyr Asp Leu Ser	Val Leu Gln Lys Pro Gln
500		505 510

<210> 68
 <211> 410
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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cttatctata tgggtgcttg ggtagggatt actctcccca gcatccaaa 200

aaaggnatgt attggngngc gccattgaat acagatggga gactgttgga 250

gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300

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taacctgacc 410

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtggtc atgggtggtg ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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catcagcaaa ccgtctgtgg ttcagctcaa ctggagaggg tt 42

<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

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 ccgtgtttgc tatgccgatg ctgtcctagt ggaacaact ccactgtaac 200
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 atgaattcag agaaaaaaa aaaaaaa 3127

<210> 73
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 73
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 35 40 45
 Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly
 50 55 60
 Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
 65 70 75
 Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val
 80 85 90
 Tyr Arg Leu Cys Phe Gly Leu Ala Met Phe Tyr Leu Leu Leu Ser
 95 100 105
 Leu Leu Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala
 110 115 120
 Val His Asn Gly Phe Trp Phe Phe Lys Phe Ala Ala Ala Ile Ala
 125 130 135
 Ile Ile Ile Gly Ala Phe Phe Ile Pro Glu Gly Thr Phe Thr Thr
 140 145 150
 Val Trp Phe Tyr Val Gly Met Ala Gly Ala Phe Cys Phe Ile Leu
 155 160 165
 Ile Gln Leu Val Leu Leu Ile Asp Phe Ala His Ser Trp Asn Glu
 170 175 180
 Ser Trp Val Glu Lys Met Glu Glu Gly Asn Ser Arg Cys Trp Tyr
 185 190 195
 Ala Ala Leu Leu Ser Ala Thr Ala Leu Asn Tyr Leu Leu Ser Leu
 200 205 210
 Val Ala Ile Val Leu Phe Phe Val Tyr Tyr Thr His Pro Ala Ser
 215 220 225
 Cys Ser Glu Asn Lys Ala Phe Ile Ser Val Asn Met Leu Leu Cys
 230 235 240
 Val Gly Ala Ser Val Met Ser Ile Leu Pro Lys Ile Gln Glu Ser
 245 250 255
 Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Val Ile Thr Val Tyr
 260 265 270
 Thr Met Tyr Leu Thr Trp Ser Ala Met Thr Asn Glu Pro Glu Thr
 275 280 285

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Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	
				305					310					315	
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	
				320					325					330	
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	
				335					340					345	
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg	
				350					355					360	
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val	
				365					370					375	
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	
				380					385					390	
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr	
				395					400					405	
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp	
				410					415					420	
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val	
				425					430					435	
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg	
				440					445					450	
Asp	Phe	Asp													

<210> 74
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 48, 163
 <223> unknown base

<400> 74
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 cgttgtggag atggggagcg tccctggggc tgtgctccat ggcgagctgg 100
 ataccatggt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150
 tagtggaaac aantccactg taactagatt gatctatgca cttttcttgc 200
 ttgttgagat atgtgtagct tgtgtaatgt tgataaccagg aatggaagaa 250
 caactgaata agattcctgg attttgtgag aatgagaaaag gtgttgtccc 300
 ttgtaacatt ttggttggct ataaagctgt atatcgtttg tgctttgggt 350
 tggctatggt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

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tgctgcagca attgcaatta ttattggggc 480

<210> 75
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323
<223> unknown base

<400> 75
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cgagctggat accangtttg tgtggaagtg ccccggtgtt gntatgccga 100
tgctgtccta gtggaacaa ntccactgta attagattga tnatgcact 150
ttntntgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250
gttgctccctt gtaacatttt ggttggctat aaagctgtat atngtttttg 300
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350
tgaagagtag cagtgatcct agagctgcaag tgcacaatgg attttggttt 400
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 48
<223> unknown base

<400> 76
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gagatgggga ggcctccttg ggttgtgctc catggcgagc tggataccat 100
gttttgtgtg aagtgccccg tgtttgctat gccgatgctg toctagtgga 150
aacaactcca ctgtaactag attgatctat gcacttttct tgotttgttg 200
agtatgtgta gotttgttaa tgttgatacc aggaatggaa gaacaactga 250
ataagattcc tggattttgt gagaatgaga aaggtgttgt cccttgtaac 300
attttggttg gctataaagc tgtatatcgt ttgtgotttg gtttggctat 350
gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagtg 400
atcctagagc tgcagtgcac aatggatttt ggttctttaa atttgcgtca 450
gcaattgcaa ttattattgg ggc 473

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COFFEE

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caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150
gaaaggtggt gtcccttctg aacatttttg gttggctata aagctgtata 200
tcgttttgtc tttggttttg ctatgttcta tcttcttcto tctttactaa 250
tgatcaaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300
ttttggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350
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cagggtgctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550
tgtctttagt tgctatcgtc ctgtctcttg tctactacac tcatccagcc 600
agttgttcoag aaaacaagcg gttcatcagt gtcaacatgc tcctctgcgt 650
tggtactttc gtaatg 666
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<220>
<223> Synthetic oligonucleotide probe

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<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence
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<400> 79
gtcaacatgc tcctctgc 18
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77

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
aatccattgt gcactgcagc tctagg 26

<210> 81
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
gagcatgccca ccaactggact gac 23

<210> 82
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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gcac 54

<210> 83
<211> 3906
<212> DNA
<213> Homo sapiens

<400> 83
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cgcgaggcct tcggcaaaagg cagtcgagtg tttgcagacc ggggcgagtc 150
ctgtgaaagc agataaaaga aaacatttat taacgtgtca ttacgagggg 200
agcgcgccgc cggggctgtc gcactccccg cggaacattt ggctccctcc 250
agctccgaga gaggagaaga agaaagcgga aaagaggcag attcacgtcg 300
tttcagcca agtggaacct atcgatggcc ctccctgaatt tatcacgata 350
tttgatttat tagcgatgcc ccctgggttg tgtgttacgc acacacacgt 400
gcacacaagg ctctggctcg ctccctccc tcgtttccag ctccctggcg 450
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tttcatgtgta atcaacatgg gaacttttag gggaacctaa taagaaatcc 3850
 caattttcag gagtggtggt gtcaataaac gctctgtggc cagtgtaaaa 3900
 gaaaaa 3906

<210> 84
 <211> 867
 <212> PRT
 <213> Homo sapiens

<400> 84
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 Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn
 35 40 45
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
 50 55 60
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
 65 70 75
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
 80 85 90
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
 95 100 105
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
 110 115 120
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
 125 130 135
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
 140 145 150
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
 155 160 165
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
 170 175 180
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
 185 190 195
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
 200 205 210
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
 215 220 225
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
 230 235 240
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
 245 250 255

Pro	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro	260	265	270
Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln	275	280	285
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met	290	295	300
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr	305	310	315
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly	320	325	330
Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val	335	340	345
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val	350	355	360
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu	365	370	375
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu	380	385	390
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met	395	400	405
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu	410	415	420
His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe	425	430	435
Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu	440	445	450
Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys	Val	455	460	465
Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro	470	475	480
Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys	485	490	495
Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp	500	505	510
Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys	515	520	525
Lys	Tyr	Lys	Ala	Ser	Tyr	Val	Arg	Ser	Arg	Ser	Ile	Arg	Ser	Val	530	535	540
Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp	545	550	555
Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala	560	565	570

Pro Glu Asp Gln Asp Asp Lys Asp Gly Gly Asp Phe Ser Gly Thr
 575 580
 Gly Gly Leu Pro Asp Tyr Ser Ala Ala Asn Pro Ile Lys Val Thr
 590 595
 His Arg Cys Tyr Ile Leu Glu Asn Asp Thr Val Gln Cys Asp Leu
 605 610
 Asp Leu Tyr Lys Ser Leu Gln Ala Trp Lys Asp His Lys Leu His
 620 625
 Ile Asp His Glu Ile Glu Thr Leu Gln Asn Lys Ile Lys Asn Leu
 635 640
 Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg Pro Glu Glu Cys
 650 655
 Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys Gly Arg Leu
 665 670
 Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly Leu Gln
 680 685
 Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys
 695 700
 Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
 710 715
 Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp
 725 730
 Gln Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr
 740 745
 Ser Ala Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu
 755 760
 Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu
 770 775
 Tyr Phe Asp Leu Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val
 785 790
 Asn Thr Leu Asp Arg Asp Val Leu Asn Gln Leu His Val Gln Leu
 800 805
 Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys Gln Cys Asn Pro Arg
 815 820
 Thr Arg Asn Met Asp Leu Asp Gly Gly Ser Tyr Glu Gln Tyr Arg
 830 835
 Gln Phe Gln Arg Arg Lys Trp Pro Glu Met Lys Arg Pro Ser Ser
 845 850
 Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp Glu Gly
 860 865

<210> 85
 <211> 19
 <212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 85
gaagccggct gtctgaatc 19

<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
ggccagctat ctccgcag 18

<210> 87
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
aagggcctgc aagagaag 18

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
cactgggaca actgtggg 18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
cagaggcaac gtggagag 18

<210> 90
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 90
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 acagcccgtc ttgtgacagt gactcccgat gagccccaga aatgacaagc 750
 gtgtcttggc agagccagca cacaagtgga tgtgaagtgc ccgtcttgac 800
 ctctcatca ggtgctgca ggcctctggc gggcagggca ctgggagagg 850
 ccctgagaat gtcccttttg ttggagaag gcagtgtgag gctgcacagt 900
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 aaaaaaaaaa aaaaaaaaaa a 971

<210> 95
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 95
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 20 25 30
 Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg 45
 35 40 45
 Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro 60
 50 55 60
 Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His 75
 65 70 75
 Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His 90
 80 85 90
 His His Pro Arg His Thr Pro His His Leu His His His His His 105
 95 100 105
 Pro His Arg His His Pro Arg His Ala Arg 115
 110 115

<210> 96
 <211> 1312
 <212> DNA
 <213> Homo sapiens

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 gtgtgacgctg ctggcctttg ccgggtactc agggctactg gctgggggtg 150
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<210> 97
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 97
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 Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 35 40 45
 Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr
 50 55 60
 Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg
 65 70 75

Ser Ile Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp
80 85 90

Lys Cys Arg Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu Glu
95 100 105

Ser Pro Ser Pro Glu Leu Ile Asp Leu Tyr Gln Lys Phe Gly Phe
110 115 120

Lys Val Phe Ser Phe Pro Ala Pro Ser His Val Val Thr Ala Thr
125 130 135

Phe Pro Tyr Thr Thr Ile Leu Ser Ile Trp Leu Ala Thr Arg Arg
140 145 150

Val His Pro Ala Leu Asp Thr Tyr Ile Lys Glu Arg Lys Leu Cys
155 160 165

Ala Tyr Pro Arg Leu Glu Ile Tyr Gln Glu Asp Gln Ile His Phe
170 175 180

Met Cys Pro Leu Ala Arg Gln Gly Asp Phe Tyr Val Pro Glu Met
185 190 195

Lys Glu Thr Glu Trp Lys Trp Arg Gly Leu Val Glu Ala Ile Asp
200 205 210

Thr Gln Val Asp Gly Thr Gly Ala Asp Thr Met Ser Asp Thr Ser
215 220 225

Ser Val Ser Leu Glu Val Ser Pro Gly Ser Arg Glu Thr Ser Ala
230 235 240

Ala Thr Leu Ser Pro Gly Ala Ser Ser Arg Gly Trp Asp Asp Gly
245 250 255

Asp Thr Arg Ser Glu His Ser Tyr Ser Glu Ser Gly Ala Ser Gly
260 265 270

Ser Ser Phe Glu Glu Leu Asp Leu Glu Gly Glu Gly Pro Leu Gly
275 280 285

Glu Ser Arg Leu Asp Pro Gly Thr Glu Pro Leu Gly Thr Thr Lys
290 295 300

Trp Leu Trp Glu Pro Thr Ala Pro Glu Lys Gly Lys Glu
305 310

<210> 98
<211> 725
<212> DNA
<213> Homo sapiens

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cccgctccat ctgctgctgc tgctgctgct cagtgcggcg gtgtgccggg 150
ctgaggtcgg gctcgaacc gaaagtccc tcgggacct ccaagtggag 200
accctggtgg agccccaga accatgtgcc gagcccgctg cttttggaga 250

185

190

195

Asn Lys Ser Lys Lys Lys
200

<210> 100
<211> 705
<212> DNA
<213> Homo sapiens

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cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150
gaggctgggc tcgaaaccga aagtccctgc cggaccctcc aagtgaggac 200
cctggtggag cccccagaac catgtgccga gcccgctgct tttggagaca 250
cgcttccatc aactacacg ggaagcttgg tagatggagc tattattgac 300
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gaagggaact cattctctct cacttgccct atggaaaacg gggatttcca 450
ccatctgtcc cagcggatgc agtgggtcag tatgacgtgg agctgattgc 500
actaatccga gccaaactact ggctaaagct ggtgaaggcg attttgcctc 550
tggtagggat ggccatggtg ccacccctct gggcctcatt gggtatcacc 600
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650
gagaaacgaa acaagagcaa aaagaaataa taataataa attttaaaaa 700
actta 705

<210> 101
<211> 543
<212> DNA
<213> Homo sapiens

<400> 101
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cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150
acctctggtg tatagaactt ggccaaaagc aggtgattcc aggtctggag 200
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggc caatcattcc 250
ttctcacttg gcctatggaa aacggggatt tocaccatct gtcccagcgg 300
atgcagtggg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350
tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

ggtgccagcc ctctctgggc tcattgggta tcacctatac agaaaggcca 450
 atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaaacag 500
 agcaaaaaga aataataaat aataaatattt aaaaaactta aaa 543
 <210> 102
 <211> 1316
 <212> DNA
 <213> Homo sapiens
 <400> 102
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 ccactgcacg acgggggctgg actgacctga aaaaaatgtc tggatttcta 150
 gagggtctga gatgctcaga atgcattgac tggggggaaa agcgaatac 200
 tattgcttcc attgctgctg gtgtactatt ttttacaggc tgggtgatta 250
 tcatagatgc agctgttatt tatccacca tgaaagattt caaccactca 300
 taccatgcct gtggtgttat agcaaccata gccctcctaa tgattaatgc 350
 agtatcgaat ggacaagtcc gaggtgatag ttacagtga ggttgtctgg 400
 gtcaaacagg tgctgcgatt tggcttttgc ttggtttcat gttggccttt 450
 ggatctctga ttgcatctat gtggattcct tttggagggt atgttgctaa 500
 agaaaaagac atagtatacc ctggaattgc tgtatttttc cagaatgcct 550
 tcatcttttt tggagggctg gtttttaagt ttggccgcac tgaagactta 600
 tggcagtga ccatctgat ttcccacagc acaacagccc tgcattgggtt 650
 tgtttgtttt tttactgctc actcccaacc ttttgaatg ccattttcta 700
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 taacttataa aatgttagag gaaactttca catgaataat ttttgtcaaa 850
 ttttatoatg gtataatttg taaaaataaa aagaaattac aaaagaattt 900
 atggatttgt caatgtaagt atttgtcata tctgaggtcc aaacacaaa 950
 tgaaagtgtc ctgaagattt aatgtgttta ttcaaatgtg gtctcttctg 1000
 tgtcaaatgt taaatgaaat ataaacattt tttagttttt aaaatatctc 1050
 gtgttcaaaa ttcttctctc ctataattgg tatttacttt taccaaaaat 1100
 tctgtgaaca tgtaatgtaa ctggcttttg aggggtctcc aaggggtgag 1150
 tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggtccctcg 1200
 tgtcccttcc atgggaagggt cttccgctgt gccctctcatt ccaagggcag 1250
 gaagatgtga ctcagccatg acacgtgggt ctggtgggat gcacagtcac 1300

tccacatcca ccaactg 1316

<210> 103

<211> 157

<212> PRT

<213> Homo sapiens

<400> 103

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Trp	Gly	Glu	Lys	Arg	Asn	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Gly	Val
			20						25					30
Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Ile	Ile	Asp	Ala	Ala	Val	Ile
				35					40					45
Tyr	Pro	Thr	Met	Lys	Asp	Phe	Asn	His	Ser	Tyr	His	Ala	Cys	Gly
				50					55					60
Val	Ile	Ala	Thr	Ile	Ala	Phe	Leu	Met	Ile	Asn	Ala	Val	Ser	Asn
				65					70					75
Gly	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Ser	Glu	Gly	Cys	Leu	Gly	Gln
				80					85					90
Thr	Gly	Ala	Arg	Ile	Trp	Leu	Phe	Val	Gly	Phe	Met	Leu	Ala	Phe
				95					100					105
Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Gly	Tyr	Val
				110					115					120
Ala	Lys	Glu	Lys	Asp	Ile	Val	Tyr	Pro	Gly	Ile	Ala	Val	Phe	Phe
				125					130					135
Gln	Asn	Ala	Phe	Ile	Phe	Phe	Gly	Gly	Leu	Val	Phe	Lys	Phe	Gly
				140					145					150
Arg	Thr	Glu	Asp	Leu	Trp	Gln								
				155										

<210> 104

<211> 545

<212> DNA

<213> Homo sapiens

<400> 104

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tggtatttcta gagggcttga gatgctcaga atgcattgac tgggggggaaa 150
agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200
tggtggatta tcatagatgc agctgttatt tatccacca tgaagattt 250
caaccactca taccatgcct gtggtgttat agcaaccata gccttcctaa 300
tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagttaa 350
ggttgtctgg gtcaaacagg tgctcgcat tggcttttcg ttggtttcat 400

gttggccttt ggatctctga ttgcatctat gtggattctt tttggaggtt 450
 atgttgctaa agaaaaagac atagtatacc ctggaattgc tgtatttttc 500
 cagaatgcct tcactctttt tggagggctg gtttttaagt ttggc 545

<210> 105
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 39, 108, 145, 179, 219, 412, 479
 <223> unknown base

<400> 105
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 agaatgcacg actgggggaa aagcgcaaat actattgctt ccattgctgc 100
 tgggtganta ttttttacag gctggtggat tatcatagat gcagntgtta 150
 tttatccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200
 atagcaacca tagccttctt aatgattaat gcagtatcga atggacaagt 250
 ccgaggtgat agttacagtg aaggttgttt gggcacaaca ggtgctcgca 300
 tttggctttt cgttggtttc atgttgccct ttggatctct gattgcatct 350
 atgtggattc tttttgagg ttatgttgct aaagaaaaag acatagtata 400
 ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450
 tggtttttaa gtttggcgc actgaagant tatggcagtg 490

<210> 106
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 26, 38, 81, 115, 207, 329, 380, 446, 449
 <223> unknown base

<400> 106
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 aatgttttga ttttttagagg gcttgagatg ntcagaatgc attgactggg 100
 ggaaaagcgc aatantattg ctttccattg ctgctggtgt actattttt 150
 acagggtggt ggattatcat agatgcagct gttatttato ccaccatgaa 200
 agatttnaac cactcatacc atgcctgttg tgttatagca accatagcct 250
 tcctaattgat taatgcagta tcgaatggac aagtcaggag tgatagttaa 300
 agtgaaggtt gtttgggtca aacaggtgnt cgcatttggc ttttcgttgg 350
 tttcatgttg gcctttggat ttctgattgn attctatgag gattcttctt 400

ggaggttatg ttgctaaaga aaaagacata gtataccctg gaattncntnt 450

atttttccag aatgcc 466

<210> 107

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356

<223> unknown base

<400> 107

tagagggcctt gagatgctca gaatgcattg actgggggga aaagcgcaat 50

antattgctt ccattgntgn tgggtgnta tttttttaca ggctgggtga 100

ttatnataga tgcagctgtt atttatccca ccataaaaga tttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcatgatng aatggacaag tccgaggtga tagttacagt gaaggttggt 250

tgggtcaaac aggtgntngc atttggcctt tngttggtt catgttggcc 300

tttgatctn tgattgcatt tatgtggatt ntttttgag gttatgttgc 350

taaaagnaaaa gacatagtat accctgt 377

<210> 108

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 12, 25, 65, 130, 437, 537

<223> unknown base

<400> 108

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ggcccgcgcg ggcngacac cgggttcogg gaaccattgc acgacggggt 100

ggactgacct gaaaaaaatg tttggatttn tagagggcct gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tgggtgacta ttttttacag gctggtggat tatcatagat gcagctgtta 250

tttatccac catgaaagat ttcaaccact cataccatgc ctgtggtgtt 300

atagcaacca tagccttct aatgattaat gcagtatoga atggacaagt 350

ccaggtgat agttacagt aaggttgtct ggggtcaaca ggtgctcgca 400

tttggtctt cgttggttc atgttggtct ttggtatct gattgcatct 450

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ccctgaatt gctgtattt tccagaatgc cttcatnttt ttggaggggc 550

tg 552

<210> 109
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 109
 gggtggaatgg tactgctgca tcc 23

<210> 110
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 110
 tgtgtgtctg tgggaaatca gatgtg 26

<210> 111
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111
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<210> 112
 <211> 3004
 <212> DNA
 <213> Homo sapiens

<400> 112
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 ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccttggtaac 150
 tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200
 aagtgcggga gaagctggat gtggtggtaa ttggcagtggt ctttgggggc 250
 ctggctgcag ctgcaattct agctaaagct ggcaagcgag tcctgggtgct 300
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 gccttgtaatt tgacacagga atccattaca ttgggcgtat ggaagagggc 400
 agcattggcc gttttatctt ggaccagatc actgaagggc agctggactg 450
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 aaaa 3004

<210> 113
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 113
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 Val Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro
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 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val
 35 40 45
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
 50 55 60
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
 65 70 75
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
 80 85 90
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
 95 100 105

Cys His Thr Phe Gly Lys Asn Gly Leu Glu Phe Asp Thr Gly Ile	110	115	120
His Tyr Ile Gly Arg Met Glu Glu Gly Ser Ile Gly Arg Phe Ile	125	130	135
Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp Trp Ala Pro Leu Ser	140	145	150
Ser Pro Phe Asp Ile Met Val Leu Glu Gly Pro Asn Gly Arg Lys	155	160	165
Glu Tyr Pro Met Tyr Ser Gly Glu Lys Ala Tyr Ile Gln Gly Leu	170	175	180
Lys Glu Lys Phe Pro Gln Glu Glu Ala Ile Ile Asp Lys Tyr Ile	185	190	195
Lys Leu Val Lys Val Val Ser Ser Gly Ala Pro His Ala Ile Leu	200	205	210
Leu Lys Phe Leu Pro Leu Pro Val Val Gln Leu Leu Asp Arg Cys	215	220	225
Gly Leu Leu Thr Arg Phe Ser Pro Phe Leu Gln Ala Ser Thr Gln	230	235	240
Ser Leu Ala Glu Val Leu Gln Gln Leu Gly Ala Ser Ser Glu Leu	245	250	255
Gln Ala Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro	260	265	270
Asn His Ser Ala Phe Ser Met His Ala Leu Leu Val Asn His Tyr	275	280	285
Met Lys Gly Gly Phe Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala	290	295	300
Phe His Thr Ile Pro Val Ile Gln Arg Ala Gly Gly Ala Val Leu	305	310	315
Thr Lys Ala Thr Val Gln Ser Val Leu Leu Asp Ser Ala Gly Lys	320	325	330
Ala Cys Gly Val Ser Val Lys Lys Gly His Glu Leu Val Asn Ile	335	340	345
Tyr Cys Pro Ile Val Val Ser Asn Ala Gly Leu Phe Asn Thr Tyr	350	355	360
Glu His Leu Leu Pro Gly Asn Ala Arg Cys Leu Pro Gly Val Lys	365	370	375
Gln Gln Leu Gly Thr Val Arg Pro Gly Leu Gly Met Thr Ser Val	380	385	390
Phe Ile Cys Leu Arg Gly Thr Lys Glu Asp Leu His Leu Pro Ser	395	400	405
Thr Asn Tyr Tyr Val Tyr Tyr Asp Thr Asp Met Asp Gln Ala Met	410	415	420

Glu Arg Tyr Val Ser Met Pro Arg Glu	Glu Ala Ala Glu His Ile
425	430
Pro Leu Leu Phe Phe Ala Phe Pro Ser	Ala Lys Asp Pro Thr Trp
440	445
Glu Asp Arg Phe Pro Gly Arg Ser Thr	Met Ile Met Leu Ile Pro
455	460
Thr Ala Tyr Glu Trp Phe Glu Glu Trp	Gln Ala Glu Leu Lys Gly
470	475
Lys Arg Gly Ser Asp Tyr Glu Thr Phe	Lys Asn Ser Phe Val Glu
485	490
Ala Ser Met Ser Val Val Leu Lys Leu	Phe Pro Gln Leu Glu Gly
500	505
Lys Val Glu Ser Val Thr Ala Gly Ser	Pro Leu Thr Asn Gln Phe
515	520
Tyr Leu Ala Ala Pro Arg Gly Ala Cys	Tyr Gly Ala Asp His Asp
530	535
Leu Gly Arg Leu His Pro Cys Val Met	Ala Ser Leu Arg Ala Gln
545	550
Ser Pro Ile Pro Asn Leu Tyr Leu Thr	Gly Gln Asp Ile Phe Thr
560	565
Cys Gly Leu Val Gly Ala Leu Gln Gly	Ala Leu Leu Cys Ser Ser
575	580
Ala Ile Leu Lys Arg Asn Leu Tyr Ser	Asp Leu Lys Asn Leu Asp
590	595
Ser Arg Ile Arg Ala Gln Lys Lys Lys	Asn
605	610

<210> 114
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<400> 114
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 gatagggctg acgctgctgc tgtgtgcggt gctgctgagc ttggcctcgg 150
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<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

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Leu	Ser	Leu	Ala	Ser	Ala	Ser	Ser	Asp	Glu	Glu	Gly	Ser	Gln	Asp
			20						25				30	

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Glu	Ser	Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val
				35					40					45
Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe
				50					55					60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu
				65					70					75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp
				80					85					90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu
				95					100					105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly
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Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp
				125					130					135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140					145					150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
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Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
				275					280					285
Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
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Leu

<210> 116
 <211> 584
 <212> DNA
 <213> Homo sapiens
 <400> 116

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<210> 119
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 119
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 35 40 45
 Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu
 50 55 60
 Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser
 65 70 75
 Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu
 80 85 90
 Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe
 95 100 105
 Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile
 110 115 120
 Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly
 125 130 135
 Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr
 140 145 150
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly
 155 160 165
 Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 170 175 180
 Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu
 185 190 195
 Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn
 200 205 210
 Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn
 215 220 225
 Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
 230 235 240

Arg Thr Arg Ser Lys Pro Val Leu Thr Gly Thr His Pro Val Asn	245	250	255
Thr Thr Val Asp Phe Gly Gly Thr Thr Ser Phe Gln Cys Lys Val	260	265	270
Arg Ser Asp Val Lys Pro Val Ile Gln Trp Leu Lys Arg Val Glu	275	280	285
Tyr Gly Ala Glu Gly Arg His Asn Ser Thr Ile Asp Val Gly Gly	290	295	300
Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val Trp Ser Arg Pro	305	310	315
Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg Ala Arg Gln	320	325	330
Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr Met Gly	335	340	345
Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro Lys	350	355	360
Pro Pro Gly Pro Pro Val Ala Ser Ser Ser Ser Ala Thr Ser Leu	365	370	375
Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile	380	385	390
Leu Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro	395	400	405
Cys Thr Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro	410	415	420
Gly Thr Ala Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu	425	430	435
Ala Ala Leu Ser Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His	440	445	450
Gly Ser Pro Ala Ala Pro Gln His Leu Leu Gly Pro Gly Pro Val	455	460	465
Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr Thr Asp Ile His Thr	470	475	480
His Thr His Thr His Ser His Thr His Ser His Val Glu Gly Lys	485	490	495
Val His Gln His Ile His Tyr Gln Cys	500		

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cgagatgacg ccgagccccc 20

<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

tgctgctcct gctgccgccc ctgctgctgg gggccttccc gccgg 45

<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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<210> 124
 <211> 1184
 <212> PRT
 <213> Homo sapiens

<400> 124
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 35 40 45
 Pro Ala Asp Thr Leu Glu Ser Pro Gly Glu Trp Thr Thr Trp Phe
 50 55 60
 Asn Ile Asp Tyr Pro Gly Gly Lys Gly Asp Tyr Glu Arg Leu Asp
 65 70 75
 Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu
 80 85 90
 Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr
 95 100 105
 Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu
 110 115 120
 Asn Arg Glu Gln Arg Pro Gly Gln Asn Cys Ser Asn Tyr Thr Val
 125 130 135
 Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg
 140 145 150
 Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys
 155 160 165
 Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu
 170 175 180
 Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys
 185 190 195
 Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly
 200 205 210

Gln Val Asn Ala	Asp Cys Asp Ala Cys	Met Cys Gln Asp Phe	Met
215		220	225
Leu His Gly Ala	Val Ser Leu Pro Gly	Gly Ala Pro Ala Ser	Gly
230		235	240
Ala Ala Ile Tyr	Leu Leu Thr Lys Thr	Pro Lys Leu Leu Thr	Gln
245		250	255
Thr Asp Ser Asp	Gly Arg Phe Arg Ile	Pro Gly Leu Cys Pro	Asp
260		265	270
Gly Lys Ser Ile	Leu Lys Ile Thr Lys	Val Lys Phe Ala Pro	Ile
275		280	285
Val Leu Thr Met	Pro Lys Thr Ser Leu	Lys Ala Ala Thr Ile	Lys
290		295	300
Ala Glu Phe Val	Arg Ala Glu Thr Pro	Tyr Met Val Met Asn	Pro
305		310	315
Glu Thr Lys Ala	Arg Arg Ala Gly Gln	Ser Val Ser Leu Cys	Cys
320		325	330
Lys Ala Thr Gly	Lys Pro Arg Pro Asp	Lys Tyr Phe Trp Tyr	His
335		340	345
Asn Asp Thr Leu	Leu Asp Pro Ser Leu	Tyr Lys His Glu Ser	Lys
350		355	360
Leu Val Leu Arg	Lys Leu Gln Gln His	Gln Ala Gly Glu Tyr	Phe
365		370	375
Cys Lys Ala Gln	Ser Asp Ala Gly Ala	Val Lys Ser Lys Val	Ala
380		385	390
Gln Leu Ile Val	Thr Ala Ser Asp Glu	Thr Pro Cys Asn Pro	Val
395		400	405
Pro Glu Ser Tyr	Leu Ile Arg Leu Pro	His Asp Cys Phe Gln	Asn
410		415	420
Ala Thr Asn Ser	Phe Tyr Tyr Asp Val	Gly Arg Cys Pro Val	Lys
425		430	435
Thr Cys Ala Gly	Gln Gln Asp Asn Gly	Ile Arg Cys Arg Asp	Ala
440		445	450
Val Gln Asn Cys	Cys Gly Ile Ser Lys	Thr Glu Glu Arg Glu	Ile
455		460	465
Gln Cys Ser Gly	Tyr Thr Leu Pro Thr	Lys Val Ala Lys Glu	Cys
470		475	480
Ser Cys Gln Arg	Cys Thr Glu Thr Arg	Ser Ile Val Arg Gly	Arg
485		490	495
Val Ser Ala Ala	Asp Asn Gly Glu Pro	Met Arg Phe Gly His	Val
500		505	510
Tyr Met Gly Asn	Ser Arg Val Ser Met	Thr Gly Tyr Lys Gly	Thr
515		520	525

Phe Thr Leu His Val Pro Gln Asp Thr	Glu Arg Leu Val Leu Thr
530	535 540
Phe Val Asp Arg Leu Gln Lys Phe Val	Asn Thr Thr Lys Val Leu
545	550 555
Pro Phe Asn Lys Lys Gly Ser Ala Val	Phe His Glu Ile Lys Met
560	565 570
Leu Arg Arg Lys Glu Pro Ile Thr Leu	Glu Ala Met Glu Thr Asn
575	580 585
Ile Ile Pro Leu Gly Glu Val Val Gly	Glu Asp Pro Met Ala Glu
590	595 600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr	Arg Gln Asn Gly Glu Pro
605	610 615
Tyr Ile Gly Lys Val Lys Ala Ser Val	Thr Phe Leu Asp Pro Arg
620	625 630
Asn Ile Ser Thr Ala Thr Ala Ala Gln	Thr Asp Leu Asn Phe Ile
635	640 645
Asn Asp Glu Gly Asp Thr Phe Pro Leu	Arg Thr Tyr Gly Met Phe
650	655 660
Ser Val Asp Phe Arg Asp Glu Val Thr	Ser Glu Pro Leu Asn Ala
665	670 675
Gly Lys Val Lys Val His Leu Asp Ser	Thr Gln Val Lys Met Pro
680	685 690
Glu His Ile Ser Thr Val Lys Leu Trp	Ser Leu Asn Pro Asp Thr
695	700 705
Gly Leu Trp Glu Glu Glu Gly Asp Phe	Lys Phe Glu Asn Gln Arg
710	715 720
Arg Asn Lys Arg Glu Asp Arg Thr Phe	Leu Val Gly Asn Leu Glu
725	730 735
Ile Arg Glu Arg Arg Leu Phe Asn Leu	Asp Val Pro Glu Ser Arg
740	745 750
Arg Cys Phe Val Lys Val Arg Ala Tyr	Arg Ser Glu Arg Phe Leu
755	760 765
Pro Ser Glu Gln Ile Gln Gly Val Val	Ile Ser Val Ile Asn Leu
770	775 780
Glu Pro Arg Thr Gly Phe Leu Ser Asn	Pro Arg Ala Trp Gly Arg
785	790 795
Phe Asp Ser Val Ile Thr Gly Pro Asn	Gly Ala Cys Val Pro Ala
800	805 810
Phe Cys Asp Asp Gln Ser Pro Asp Ala	Tyr Ser Ala Tyr Val Leu
815	820 825
Ala Ser Leu Ala Gly Glu Glu Leu Gln	Ala Val Glu Ser Ser Pro
830	835 840

Lys Phe Asn Pro Asn Ala Ile Gly Val	Pro Gln Pro Tyr Leu Asn
845	850
Lys Leu Asn Tyr Arg Arg Thr Asp His	Glu Asp Pro Arg Val Lys
860	865
Lys Thr Ala Phe Gln Ile Ser Met Ala	Lys Pro Arg Pro Asn Ser
875	880
Ala Glu Glu Ser Asn Gly Pro Ile Tyr	Ala Phe Glu Asn Leu Arg
890	895
Ala Cys Glu Glu Ala Pro Pro Ser Ala	Ala His Phe Arg Phe Tyr
905	910
Gln Ile Glu Gly Asp Arg Tyr Asp Tyr	Asn Thr Val Pro Phe Asn
920	925
Glu Asp Asp Pro Met Ser Trp Thr Glu	Asp Tyr Leu Ala Trp Trp
935	940
Pro Lys Pro Met Glu Phe Arg Ala Cys	Tyr Ile Lys Val Lys Ile
950	955
Val Gly Pro Leu Glu Val Asn Val Arg	Ser Arg Asn Met Gly Gly
965	970
Thr His Arg Arg Thr Val Gly Lys Leu	Tyr Gly Ile Arg Asp Val
980	985
Arg Ser Thr Arg Asp Arg Asp Gln Pro	Asn Val Ser Ala Ala Cys
995	1000
Leu Glu Phe Lys Cys Ser Gly Met Leu	Tyr Asp Gln Asp Arg Val
1010	1015
Asp Arg Thr Leu Val Lys Val Ile Pro	Gln Gly Ser Cys Arg Arg
1025	1030
Ala Ser Val Asn Pro Met Leu His Glu	Tyr Leu Val Asn His Leu
1040	1045
Pro Leu Ala Val Asn Asn Asp Thr Ser	Glu Tyr Thr Met Leu Ala
1055	1060
Pro Leu Asp Pro Leu Gly His Asn Tyr	Gly Ile Tyr Thr Val Thr
1070	1075
Asp Gln Asp Pro Arg Thr Ala Lys Glu	Ile Ala Leu Gly Arg Cys
1085	1090
Phe Asp Gly Thr Ser Asp Gly Ser Ser	Arg Ile Met Lys Ser Asn
1100	1105
Val Gly Val Ala Leu Thr Phe Asn Cys	Val Glu Arg Gln Val Gly
1115	1120
Arg Gln Ser Ala Phe Gln Tyr Leu Gln	Ser Thr Pro Ala Gln Ser
1130	1135
Pro Ala Ala Gly Thr Val Gln Gly Arg	Val Pro Ser Arg Arg Gln
1145	1150

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala
 1160 1165 1170

Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn
 1175 1180

<210> 125

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

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<210> 126

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ccattgtgca ggtcagggtca cag 23

<210> 127

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

ctggagcaag tgctcagctg cctgtggtca gactggggtc 40

<210> 128

<211> 2819

<212> DNA

<213> Homo sapiens

<400> 128

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 ctacctacc gtaacgatac atacatatgt gtatatatat gtaaacataga 200
 caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250
 aaaaagaatt tagagatgta tttgtcaaga tcctgtgcga ttcatgccct 300
 ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350
 attatgattt gtgtaagact cagatttaca cggaagaagg gaaagtttgg 400
 gattacatgg cctgccagcc ggaatccacg gacatgacaa aatatctgaa 450

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[illegible]

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<210> 130
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 130
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<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 131
ttctgagatc cctcatcctc 20

<210> 132
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 132
agggttcaggg acagcaagtt tggg 24

<210> 133
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 133
ttgtctggac ctgggctacg gaattggctt ccctctacgg acagctggat 50

<210> 134
<211> 1493
<212> DNA
<213> Homo sapiens

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cggggcgagg tgtcctcatg acttctcttg tggaccatgt cgtgatctt 150
ttttgcctgc gtggtacggg taagggatgg actgccccto tcagcctcta 200
ctgatTTTTA ccacacccaa gatttttttg aatggaggag acgggtcaag 250
agtttagcct tgcgactggc ccagtatcca ggtcgagggt ctgcagaagg 300

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gcataaaaaa	ctgaggctga	tttagtcagg	gcaaaacccat	ttactttaca	1250
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aaatctaaag	tggtttattaa	aaaaaaaaaa	aaaaaaaaaa	aag	1493

<210> 135

<211> 228

<212> PRT

<213> Homo sapiens

<400> 135

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly
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Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe
20 25 30

Leu Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Ala
35 40 45

1000 900 800 700 600 500 400 300 200 100 0

121

tgtctcctgg tcttaagctc agcacttctt gtcttctctc gaaccctggg 1550
 gctcactcgc ttgacctgc tgggtgactt tggacgcttc aactggctgg 1600
 gcaatttcta cattgtgttc ctctacaacg cagcctttgc aggcctcaac 1650
 acactctgtc tggagaagac ctctactgca gctgtcggg cagagctgat 1700
 ccgggccttt gggctggaca gactgccgct gcccgctctc ggtttccccc 1750
 aggcacttag gaagaccag caccagtac ctccagctgg ggtgggaag 1800
 gaaaaaactg gacactgcc tctgctgcct aggcctggag ggaagcccaa 1850
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<210> 138

<211> 489

<212> PRT

<213> Homo sapiens

<400> 138

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Phe	His	Glu	Arg	Ile	Arg	Glu	Cys	Ile	Ile	Ser	Thr	Leu	Leu	Phe
			20					25					30	
Ala	Thr	Leu	Tyr	Ile	Leu	Cys	His	Ile	Phe	Leu	Thr	Arg	Phe	Lys
			35					40					45	
Lys	Pro	Ala	Glu	Phe	Thr	Thr	Val	Asp	Asp	Glu	Asp	Ala	Thr	Val
			50					55					60	
Asn	Lys	Ile	Ala	Leu	Glu	Leu	Cys	Thr	Phe	Thr	Leu	Ala	Ile	Ala
			65					70					75	
Leu	Gly	Ala	Val	Leu	Leu	Leu	Pro	Phe	Ser	Ile	Ile	Ser	Asn	Glu
			80					85					90	
Val	Leu	Leu	Ser	Leu	Pro	Arg	Asn	Tyr	Tyr	Ile	Gln	Trp	Leu	Asn
			95					100					105	
Gly	Ser	Leu	Ile	His	Gly	Leu	Trp	Asn	Leu	Val	Phe	Leu	Phe	Pro
			110					115					120	
Asn	Leu	Ser	Leu	Ile	Phe	Leu	Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr

125					130					135				
Glu Ser Glu Gly	Phe Ala Gly Ser Arg	Lys Gly Val Leu Gly	Arg											
	140			145									150	
Val Tyr Glu Thr	Val Val Met Leu Met	Leu Leu Thr Leu Leu	Val											
	155			160									165	
Leu Gly Met Val	Trp Val Ala Ser Ala	Ile Val Asp Lys Asn	Lys											
	170			175									180	
Ala Asn Arg Glu	Ser Leu Tyr Asp Phe	Trp Glu Tyr Tyr Leu	Pro											
	185			190									195	
Tyr Leu Tyr Ser	Cys Ile Ser Phe Leu	Gly Val Leu Leu Leu	Leu											
	200			205									210	
Val Cys Thr Pro	Leu Gly Leu Ala Arg	Met Phe Ser Val Thr	Gly											
	215			220									225	
Lys Leu Leu Val	Lys Pro Arg Leu Leu	Glu Asp Leu Glu Glu	Gln											
	230			235									240	
Leu Tyr Cys Ser	Ala Phe Glu Glu Ala	Ala Leu Thr Arg Arg	Ile											
	245			250									255	
Cys Asn Pro Thr	Ser Cys Trp Leu Pro	Leu Asp Met Glu Leu	Leu											
	260			265									270	
His Arg Gln Val	Leu Ala Leu Gln Thr	Gln Arg Val Leu Leu	Glu											
	275			280									285	
Lys Arg Arg Lys	Ala Ser Ala Trp Gln	Arg Asn Leu Gly Tyr	Pro											
	290			295									300	
Leu Ala Met Leu	Cys Leu Leu Val Leu	Thr Gly Leu Ser Val	Leu											
	305			310									315	
Ile Val Ala Ile	His Ile Leu Glu Leu	Leu Ile Asp Glu Ala	Ala											
	320			325									330	
Met Pro Arg Gly	Met Gln Gly Thr Ser	Leu Gly Gln Val Ser	Phe											
	335			340									345	
Ser Lys Leu Gly	Ser Phe Gly Ala Val	Ile Gln Val Val Leu	Ile											
	350			355									360	
Phe Tyr Leu Met	Val Ser Ser Val Val	Gly Phe Tyr Ser Ser	Pro											
	365			370									375	
Leu Phe Arg Ser	Leu Arg Pro Arg Trp	His Asp Thr Ala Met	Thr											
	380			385									390	
Gln Ile Ile Gly	Asn Cys Val Cys Leu	Leu Val Leu Ser Ser	Ala											
	395			400									405	
Leu Pro Val Phe	Ser Arg Thr Leu Gly	Leu Thr Arg Phe Asp	Leu											
	410			415									420	
Leu Gly Asp Phe	Gly Arg Phe Asn Trp	Leu Gly Asn Phe Tyr	Ile											
	425			430									435	
Val Phe Leu Tyr	Asn Ala Ala Phe Ala	Gly Leu Thr Thr Leu	Cys											

	440		445		450
Leu Val Lys Thr	Phe Thr Ala Ala Val	Arg Ala Glu Leu Ile	Arg		
	455		460		465
Ala Phe Gly Leu	Asp Arg Leu Pro Leu	Pro Val Ser Gly Phe	Pro		
	470		475		480
Gln Ala Ser Arg	Lys Thr Gln His Gln				
	485				

<210> 139
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 53, 57
 <223> unknown base

<400> 139
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 tcatgtctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150
 gagaacagct attccacgag aggatccgcg agtgtattat atcaaacatt 200
 ctgtttgcaa cactgtacat cctctgcoac atcttcctga cccgcttcaa 250
 gaagcctgct gagttcacca cagtggatga tgaagatgcc accg 294

<210> 140
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 197, 349
 <223> unknown base

<400> 140
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 gagccccaga ctgccccgag tttctgtcgc aggctgcgag gaaaggcccc 150
 taggtggtgt ctggtgcttg gcggcggcgg cttcctcccc gttgtentcc 200
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 cacctgacta cgaagtgcata tccgtgcgag aacagctatt ccacgagagg 300
 atccgcgagt gtattatata aacactttctg ttgcaaacac tgtacatont 350
 ctgcacatc ttcctgaccc gcttcaagaa gcctgctgag ttcaccacag 400
 tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450

tttaccctgg caattgcctt ggggtgctgc ctgctcctgc ccttctccat 500
catcagcaat gaggtgctgc actccc 526

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
gactgtatct gagcccccaga ctgc 24

<210> 142
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 142
tcagcaatga ggtgctgctc 20

<210> 143
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 143
tgaggaagat gagggacagg ttgg 24

<210> 144
<211> 50
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 144
tatggaagca cctgactacg aagtgcctatc cgtgcgagaa cagctattcc 50

<210> 145
<211> 685
<212> DNA
<213> Homo sapiens

<400> 145
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tggtccaggt cttcatgctg ctgtgggtga tattactggt cctggctcct 150

gtcagtggac agtttgcaag gacaccacag ccattattt tcctccagcc 200

tccatggacc acagtottcc aaggagagag agtgacccto acttgcaagg 250

gatttcgctt ctactcacca cagaaaaaaa aatggtacca tcggtacctt 300
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 aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 146
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 35 40 45
 Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg
 50 55 60
 Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu
 65 70 75
 Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser
 80 85 90
 Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Glu Met Gly
 95 100 105
 Phe Pro His Ala Ala Gln Ala Asn Val Glu Leu Leu Gly Ser Ser
 110 115 120

Asp Leu Leu Thr

<210> 147
 <211> 1621
 <212> DNA
 <213> Homo sapiens

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 cgcgcgccgc gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaacat ggctccgag aacctgagca ccttttgcct gttgctgcta 200
 tacctcatcg gggcggatg tgccggacga gatttctata agatcttggg 250
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 tggtcacaag gtacatatct cccgggataa gatcaccagg ccaggagcga 1050
 agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatatc 1100
 aagggctctt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150
 aacagaggaa gcgagagaag gtatcaaca gctactgaaa caagggctag 1200
 tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250
 gactttgttt aaaataagtg aataagcgat atttattatc tgcagggttt 1300
 ttttgtgtgt gttttgttt ttattttcaa tatgcaagtt aggcctaatt 1350
 tttttatcta atgatcatca tgaatgaat aagagggtct aagaatttgt 1400
 ccatttgcac tcggaaaaga atgaccagca aaaggtttac taatacctct 1450
 ccctttgggg attttaatgtc tgggtgtgcc gcctgagttt caagaattaa 1500
 agctgcaaga ggactccagg agcaaaagaa acacaatata gaggggttga 1550
 gttgttagca atttcattca aaatgccaac tggagaagtc tgttttttaa 1600
 tacattttgt tgtatttttt a 1621

<210> 148
 <211> 358
 <212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Tyr
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Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile
				20					25				30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala
				35					40				45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp
				50					55				60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr
				65					70				75
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr
				80					85				90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp
				95					100				105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly
				110					115				120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile
				125					130				135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn
				140					145				150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro
				155					160				165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln
				170					175				180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp
				185					190				195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu
				200					205				210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe
				215					220				225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu
				230					235				240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg
				245					250				255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser
				260					265				270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys
				275					280				285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu
				290					295				300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys
 305 310
 Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln
 320 325
 Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
 335 340
 Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
 350 355

<210> 149
 <211> 509
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> unsure
 <222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,
 482
 <223> unknown base

<400> 149
 tgggaccagg gaaccccggtg ccccccggtg gaggcctaa caggccggtg 50
 gntgcgaccg aagcggcggtg cggaggaggt tttgaggatt ttggaacag 100
 gaccgcgaca gaggaaccaa ggttcgcgag aacntgagca cnttttgcct 150
 gttgntgnta tacttcacgc gggcggtgat tgcgcgacga gatttntata 200
 agattttggg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250
 tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300
 acaagcccag gagaattcc aggatgtggg tgctgcttat gaggttntgt 350
 cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400
 aaagatggtn atcagagctc ccatggagac attttttcac acttntttgg 450
 ggattttggt ttcattgttg gaggaacccc tngtcagcaa gacagaaata 500
 ttccaagag 509

<210> 150
 <211> 1532
 <212> DNA
 <213> Homo sapiens

<400> 150
 ggcacgaggg ggcggggcag tgcggggatg cgcccgagg ccacagcctg 50
 aggcctcag gtctctgcag gtgtcgtgga ggaacctag acctgccatc 100
 ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150
 gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200
 gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250
 ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

gctatgattc taagccatt gtggacctca ttggtgccat ggagaccag 350
 tctgagccct ctgagttaga actggacgat gtcgttatca ccaaccccca 400
 cattgaggcc attctggaga atgaagactg gatcgaagat gcctcgggtc 450
 tcatgtccca ctgcattgcc atcttgaaga ttgtcacac tctgacagag 500
 aagcttgttg ccatgacaat gggctctggg gccaaagatga agacttcagc 550
 cagtgtcagc gacatcattg ttggtggcaa gcggatcagc cccagggttg 600
 atgatgttgt gaagtcgatg taccctcogt tggaccccaa actcctggac 650
 gcacggacga ctgccctgct cctgtctgtc agtcacctgg tgctggtgac 700
 aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750
 tgtcggctgc tgaggagcat ttggaagtcc ttcgagaagc agccctagct 800
 tctgagccag ataaaggcct cccaggccct gaaggcttcc tgcaggagca 850
 gtctgcaatt tagtgcctac aggccagcag ctagccatga aggccctgc 900
 cgccatccct ggatggtcca gcttagcctt ctacttttcc ctatagagt 950
 agttgttctc caccgctgga gagttcagct gtgtgtgcat agtaaacgag 1000
 gagatccccc tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050
 gagtggcagt ctaatactac agttagggga gatgccattc actctctgca 1100
 agaggagtat tgaaaaactg ttgactgtca gctttattta gctcacctag 1150
 tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200
 taaaattaga atttctggcc tctctcgatc ggtcagaatg tgtggcaatt 1250
 ctgatctgca ttttcagaag aggacaatca attgaaacta agtaggggtt 1300
 tcttcttttg gcaagacttg tactctctca cctggcctgt ttcatttatt 1350
 tgtattatct gcctggtccc tgaggcgtct gggctctctc tctcccttgc 1400
 aggtttgggt ttgaagctga ggaactacaa agttgatgat ttctttttta 1450
 tctttatgcc tgcaatttta cctagctacc actaggtgga tagtaaattt 1500
 atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 151
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 Phe Leu Ala Ser Phe Ala Ala Leu Val Leu Val Cys Arg Gln Arg
 20 25 30
 Tyr Cys Arg Pro Arg Asp Leu Leu Gln Arg Tyr Asp Ser Lys Pro

	35		40		45
Ile Val Asp Leu	Ile Gly Ala Met Glu	Thr Gln Ser Glu Pro Ser			
	50	55			60
Glu Leu Glu Leu Asp Asp Val Val Ile	Thr Asn Pro His Ile Glu				
	65	70			75
Ala Ile Leu Glu Asn Glu Asp Trp Ile	Glu Asp Ala Ser Gly Leu				
	80	85			90
Met Ser His Cys Ile Ala Ile Leu Lys	Ile Cys His Thr Leu Thr				
	95	100			105
Glu Lys Leu Val Ala Met Thr Met Gly	Ser Gly Ala Lys Met Lys				
	110	115			120
Thr Ser Ala Ser Val Ser Asp Ile Ile	Val Val Ala Lys Arg Ile				
	125	130			135
Ser Pro Arg Val Asp Asp Val Val Lys	Ser Met Tyr Pro Pro Leu				
	140	145			150
Asp Pro Lys Leu Leu Asp Ala Arg Thr	Thr Ala Leu Leu Leu Ser				
	155	160			165
Val Ser His Leu Val Leu Val Thr Arg	Asn Ala Cys His Leu Thr				
	170	175			180
Gly Gly Leu Asp Trp Ile Asp Gln Ser	Leu Ser Ala Ala Glu Glu				
	185	190			195
His Leu Glu Val Leu Arg Glu Ala Ala	Leu Ala Ser Glu Pro Asp				
	200	205			210
Lys Gly Leu Pro Gly Pro Glu Gly Phe	Leu Gln Glu Gln Ser Ala				
	215	220			225
Ile					

<210> 152
 <211> 1027
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 1017, 1020
 <223> unknown base

<400> 152
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 tcgccgctgt cccaccact gcagccatga tctccttaac ggacacgcag 100
 aaaattggaa tgggattaac aggatttga gtgtttttcc tgttcttttg 150
 aatgattctc ttttttgaca aagcactact ggctattgga aatgttttat 200
 ttgtagccgg ctggctttt gtaattggtt tagaagaac attcagattc 250
 ttcttccaaa aacataaaat gaaagctaca gggttttttc tgggtggtgt 300

Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val
65 70
Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu
80 85 90
Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val
95 100 105
Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn
110 115 120
Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn
125 130 135
Asn Met Val

<210> 154
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 66
<223> unknown base

<400> 154
gaagacgtgg cggtctcgc ctgggctggt tcccgcttc atttctcccg 50
actcagcttc ccacntggg ctttccgagg tgctttcgcc gctgtcccca 100
ccactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150
ttaaccggat ttggagtgtt tttctgttc tttggaatga ttctcttttt 200
tgacaaagca ctactggcta ttggaatgt tttatttga gccggcttgg 250
cttttghtaat tgggttagaa agaacattca gattcttctt ccaaaaacat 300
aaaatgaaag ctacaggttt ttttctgggt ggtgtatttg tagtccttat 350
tggttgccct ttgataggca tgatcttcga aatttatgga tttttctct 400
tggtc 405

<210> 155
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 155
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ccatgtgcc aagctgcc aagaggagac gccttctga gtcctggatc 100
tttcttctt ctggaatat ttgactgtg gtagttattt atttctgaat 150
aagagcgctc acgcatcatg gacctcgcg gactgctgaa gtctcagttc 200
ctgtgcacc tggcttctg ctactgttt attgcctcag ggctaatacat 250

caacaccatt cagctcttca ctctctctct ctggccatt aacaagcagc 300
tcttcggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350
gtgatgtgc tggagtgggt gtcgggcacg gaatgcacca tcttcacgga 400
cccgcgcgcc tacctcaagt atgggaagga aatgccatc gtggttctca 450
accacaagtt tgaaattgac tttctgtgtg gctggagcct gtccgaacgc 500
tttgggctgt tagggggctc caaggctctg gccagaaga agctggccta 550
tgtccaatt atcggtgga tgtggtactt caccgagatg gtcttctgtt 600
cgcgcaagt ggagcaggat cgcaagacgg ttgccaccag tttgcagcac 650
ctccgggact accccgagaa gtatttttct ctgattcact gtgagggacc 700
acggttcacg gagaagaagc atgagatcag catgcagggt gcccgggcca 750
aggggctgcc tcgcctcaag catcacctgt tgccacgaac caagggtctc 800
gccatcacgg tgaggagctt gagaaatga gtttcagctg tatatgactg 850
tacactcaat ttcagaaata atgaaaatcc aacactgctg ggagtcttaa 900
acggaagaa ataccatgca gatttgtatg ttagggagat ccaactggaa 950
gacatccctg aagacgatga cgagtgtctg gcctggctgc acaagctcta 1000
ccaggagaag gatgccttct agggaggagta ctacaggacg ggcaccttc 1050
cagagaagcc catggtgccc ccccgcgggc cctggaccc cgtgaactgg 1100
ctgttttggg cctcgctggt gctctaccct ttcttccagt tctgggtcag 1150
catgatcagg agcgggtctt cctgacgct ggccagcttc atcctcgtct 1200
tctttgtggc ctccgtggga gttcgatgga tgattggtgt gacggaaatt 1250
gacaagggtc ctgcctacgg caactctgac agcaagcaga aactgaatga 1300
ctgactcagg gaggtgtcac catccgaagg gaaccttggg gaactggtg 1350
cctctgcata tctctcttag tgggacacgg tgacaaaggc tgggtgagcc 1400
cctgtcgggc acggcggaag tcacgacctc tcacgacagg gagtctggtc 1450
tcaaggccgg atggggagga agatgttttg taatcttttt tccccatgt 1500
gcttttagtg gctttggtt tctttttgtg cgagtgtgtg tgagaatggc 1550
tgtgtggtga ggtgaaact tgttctgtga tcatagaaa ggtattttag 1600
gtgcagggg agggcagggc tggggaccga aggggacaag tcccccttc 1650
atccttttgt gctgagtttt ctgtaaccct tgggtgccag agataaagt 1700
aaaagtgcct taggtgagat gactaaatta tgccccaag aaaaaaaaa 1750
taaagtgcct ttctgggtca aaaaaaaaa a 1781

<210> 156

<211> 378
 <212> PRT
 <213> Homo sapiens

<400> 156

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	
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Val	Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	
				20					25					30	
Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	
				35					40					45	
Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	
				50					55					60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	
				65					70					75	
Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	
				80					85					90	
Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	
				95					100					105	
Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	
				110					115					120	
Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	
				125					130					135	
Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	
				140					145					150	
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	
				155					160					165	
Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Arg	Leu	Lys	His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Ala	Ile	Thr	Val	Arg	Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	
				215					220					225	
Tyr	Asp	Cys	Thr	Leu	Asn	Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	
				230					235					240	
Leu	Gly	Val	Leu	Asn	Gly	Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	
				245					250					255	
Arg	Arg	Ile	Pro	Leu	Glu	Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	
				260					265					270	
Ser	Ala	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Phe	Gln	
				275					280					285	
Glu	Glu	Tyr	Tyr	Arg	Thr	Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val	

290	295	300
Pro Pro Arg Arg Pro Trp Thr Leu Val	Asn Trp Leu Phe Trp Ala	
305	310	315
Ser Leu Val Leu Tyr Pro Phe Phe Gln	Phe Leu Val Ser Met Ile	
320	325	330
Arg Ser Gly Ser Ser Leu Thr Leu Ala	Ser Phe Ile Leu Val Phe	
335	340	345
Phe Val Ala Ser Val Gly Val Arg Trp	Met Ile Gly Val Thr Glu	
350	355	360
Ile Asp Lys Gly Ser Ala Tyr Gly Asn	Ser Asp Ser Lys Gln Lys	
365	370	375
Leu Asn Asp		

<210> 157
 <211> 1849
 <212> DNA
 <213> Homo sapiens

<400> 157
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 acggaaggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150
 tactgattcc caaatgatg atgttgaaat tggtttatata attgacattc 200
 agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250
 gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa 300
 tgtggtaggt tggtaacaaat tccgtcgtca ttcagatcag atcatgacgt 350
 ttagagagag gctgcttcac aaaaaactgc aggagcattt tcaaaacca 400
 gaccttgttt ttctgctatt aacaccaagt ataataacag aaagctgctc 450
 tactcatcga ctggaacatt ctttatataa acctcaaaaa ggactttttc 500
 acagggtacc tttagtggtt gccaatctgg gcatgtctga acaactgggt 550
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 acaaacacac agctctaaat tttttgaaga agatggatcc ttaaaggagg 650
 tacataagat aaatgaaatg tatgcttcat tacaagagga attaaagagt 700
 atatgcaaaa aagtgaaga cagtgaacaa gcagtagata aactagtaaa 750
 ggatgtaaac agattaaaac gagaaattga gaaaaggaga ggagcacaga 800
 ttcaggcagc aagagagaag aacatccaaa aagacctca ggagaacatt 850
 tttctttgtc aggcattacg gacctttttt ccaaattctg aattttcttc 900
 ttcattgtgt atgtctttaa aaaatagaca tgtttctaaa agtagctgta 950

actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa 1000
 cacactgaca ttctgaagc tagtcagct agtacaccac aaatcattaa 1050
 gcataaagcc ttagacttag atgacagatg gcaattcaag agatctoggt 1100
 tgttagatag acaagacaaa cgatctaaag caaatactgg tagtagtaac 1150
 caagataaag catocaaaat gagcagccca gaaacagatg aagaaattga 1200
 aaagatgaag gggtttggtg aatattcacg gtctctaca ttttgatcct 1250
 tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac 1300
 atttctattg ttttactat gttgagctac ttgcagtaag ttcatttggt 1350
 tttactatgt tcacctgttt gcagtaatac acagataaact cttagtgcac 1400
 ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc 1450
 tttttttcac ctttactaa gttgttgagg ggaaggctta cacagacaca 1500
 ttctttagaa ttggaaggt gagaccaggc acagtggcto acacctgtaa 1550
 tccagcact tagggaagac aagtcaggag gattgattga agctaggagt 1600
 tagagaccag cctgggcaac gtattgagac catgtctatt aaaaaataaa 1650
 atggaagac aagaatagcc ttattttcaa aatatggaaa gaaatttata 1700
 tgaataatta tctgagcat taaaattctc cttaatgtat acttttttag 1750
 aagtacatta tggctagagt tgccagataa aatgctggat atcatgcaat 1800
 aaatttgcaa aacatcatct aaaattttaa aaaaaaaaaa aaaaaaaaaa 1849

<210> 158

<211> 409

<212> PRT

<213> Homo sapiens

<400> 158

Met	Glu	Gly	Glu	Ser	Thr	Ser	Ala	Val	Leu	Ser	Gly	Phe	Val	Leu
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Gly	Ala	Leu	Ala	Phe	Gln	His	Leu	Asn	Thr	Asp	Ser	Asp	Thr	Glu
				20					25					30
Gly	Phe	Leu	Leu	Gly	Glu	Val	Lys	Gly	Glu	Ala	Lys	Asn	Ser	Ile
				35					40					45
Thr	Asp	Ser	Gln	Met	Asp	Asp	Val	Glu	Val	Val	Tyr	Thr	Ile	Asp
				50					55					60
Ile	Gln	Lys	Tyr	Ile	Pro	Cys	Tyr	Gln	Leu	Phe	Ser	Phe	Tyr	Asn
				65					70					75
Ser	Ser	Gly	Glu	Val	Asn	Glu	Gln	Ala	Leu	Lys	Lys	Ile	Leu	Ser
				80					85					90
Asn	Val	Lys	Lys	Asn	Val	Val	Gly	Trp	Tyr	Lys	Phe	Arg	Arg	His
				95					100					105

Ser Asp Gln Ile	Met Thr Phe Arg Glu	Arg Leu Leu His Lys Asn
110		115 120
Leu Gln Glu His	Phe Ser Asn Gln Asp	Leu Val Phe Leu Leu Leu
125		130 135
Thr Pro Ser Ile	Ile Thr Glu Ser Cys	Ser Thr His Arg Leu Glu
140		145 150
His Ser Leu Tyr	Lys Pro Gln Lys Gly	Leu Phe His Arg Val Pro
155		160 165
Leu Val Val Ala	Asn Leu Gly Met Ser	Glu Gln Leu Gly Tyr Lys
170		175 180
Thr Val Ser Gly	Ser Cys Met Ser Thr	Gly Phe Ser Arg Ala Val
185		190 195
Gln Thr His Ser	Ser Lys Phe Phe Glu	Glu Asp Gly Ser Leu Lys
200		205 210
Glu Val His Lys	Ile Asn Glu Met Tyr	Ala Ser Leu Gln Glu Glu
215		220 225
Leu Lys Ser Ile	Cys Lys Lys Val Glu	Asp Ser Glu Gln Ala Val
230		235 240
Asp Lys Leu Val	Lys Asp Val Asn Arg	Leu Lys Arg Glu Ile Glu
245		250 255
Lys Arg Arg Gly	Ala Gln Ile Gln Ala	Ala Arg Glu Lys Asn Ile
260		265 270
Gln Lys Asp Pro	Gln Glu Asn Ile Phe	Leu Cys Gln Ala Leu Arg
275		280 285
Thr Phe Phe Pro	Asn Ser Glu Phe Leu	His Ser Cys Val Met Ser
290		295 300
Leu Lys Asn Arg	His Val Ser Lys Ser	Ser Cys Asn Tyr Asn His
305		310 315
His Leu Asp Val	Val Asp Asn Leu Thr	Leu Met Val Glu His Thr
320		325 330
Asp Ile Pro Glu	Ala Ser Pro Ala Ser	Thr Pro Gln Ile Ile Lys
335		340 345
His Lys Ala Leu	Asp Leu Asp Asp Arg	Trp Gln Phe Lys Arg Ser
350		355 360
Arg Leu Leu Asp	Thr Gln Asp Lys Arg	Ser Lys Ala Asn Thr Gly
365		370 375
Ser Ser Asn Gln	Asp Lys Ala Ser Lys	Met Ser Ser Pro Glu Thr
380		385 390
Asp Glu Glu Ile	Glu Lys Met Lys Gly	Phe Gly Glu Tyr Ser Arg
395		400 405
Ser Pro Thr Phe		

<210> 159
 <211> 2651
 <212> DNA
 <213> Homo sapiens

<400> 159
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 cgcgcgccac accctctgag gtccccgcgg cgcctgccac ccttccctcc 150
 ttccccgcgt ccccgccctg ccggccagtc agcttgccgg gttcgtgcc 200
 ccgcgaaacc ccgaggtcac cagcccgccg ctctgcttcc ctgggcgcgg 250
 cgcgcctcc acgcctcct tctccccg ccggcgccct ggacccgggg 300
 accgttgct gacgcgaggc ccagctctac ttttcgccc gcgtctctcc 350
 cgcctgctg cctcttccac caactccaac tcttcttcc tccagctcca 400
 ctgcgtagtc cccgactccg ccagccctcg gcccgctgcc gtacgcgcgc 450
 ttcccgctcg gtcccaaagg tgggaacgcg tccgccccg cccgcaccat 500
 ggcacggttc ggcctgcccg cgcctctctg caccctggca gtgctcagcg 550
 ccgcgctgct ggcgtccgag ctcaagtcga aaagttgctc ggaagtgcga 600
 cgtctttacg tgtccaaagg cttcaacaag aacgatgccc cctccaaga 650
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 agtgtgtgca gcgaacagtg caatcatttg caagctgtct ttgcttcacg 800
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 aatccctgaa tgatatgtt gtgaagacat atggccattt atacatgcaa 900
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 tcctggagcg gatgttcgcg ctggtgaact ccagtagca ctttacagat 1050
 gagtatctgg aatgtgtgag caagtatacg gacgagctga agcccttcgg 1100
 agatgtccct cgcgaattga agctccaggt tactcgtgct tttgtagcag 1150
 ccggtacttt cgtcgaaggc ttacgcggtg cgggagatgt cgtgagcaag 1200
 gtctccgttg taaacccac agcccagtg acccatgccc tgttgaaagt 1250
 gatctactgc tccactgcc ggggtctcgt gactgtgaag ccattgtaca 1300
 actactgctc aaacatcatg agaggctgtt tggccaacca agggatctc 1350
 gattttgaat ggaacaatt catagatgct atgctgatgg tggcagagag 1400
 gctagagggt cctttcaaca ttgaatcggt catggatccc atcgatgtga 1450

agatttctga tgctattatg aacatgcagc ataatagtgt tcaagtgtct 1500
 cagaagggtt tccagggatg tggaccccc aagcccctcc cagctggacg 1550
 aatttctcgt tccatctctg aaagtgcctt cagtgtctcg ttcagaccac 1600
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 ggttgacacc agcaaaaccag acatactgat ccttcgtcaa atcatggctc 1900
 ttcgagtgat gaccagcaag atgaagaatg catacaatgg gaacgacgtg 1950
 gacttctttg atatcagtga tgaaagtagt ggagaaggaa gtggaagtgg 2000
 ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc 2050
 atgctgggaa gagtgccaat gagaagccg acagtgtctg tgctcgtcct 2100
 ggggcacagg octacctct cactgtcttc tgcactttgt tctcggttat 2150
 gcagagagag tggagataat tctcaaacct tgagaaaaag tgtcatcaa 2200
 aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc 2250
 tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg 2300
 ttttaagaag gctgactttg ttttctcatt cagttttggg aggaaaaggg 2350
 actgtgcatt gagttgggtc ctgctccccc aaacatgttt aaacgtggct 2400
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 ctctattatt tgtttgatg tttttttctc atttcgtttg tgggtttttt 2500
 ttccaactg tgatctcgcc ttgtttctta caagcaaacc agggctccctt 2550
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 agcaggtttt atttatcatg ttatcttatt aaaagaaaaa gcccaaaaaa 2650

c 2651

<210> 160

<211> 556

<212> PRT

<213> Homo sapiens

<400> 160

Met	Ala	Arg	Phe	Gly	Leu	Pro	Ala	Leu	Leu	Cys	Thr	Leu	Ala	Val
1				5					10					15
Leu	Ser	Ala	Ala	Leu	Leu	Ala	Ala	Glu	Leu	Lys	Ser	Lys	Ser	Cys
				20					25					30
Ser	Glu	Val	Arg	Arg	Leu	Tyr	Val	Ser	Lys	Gly	Phe	Asn	Lys	Asn

					35					40					45
Asp	Ala	Pro	Leu	His	Glu	Ile	Asn	Gly	Asp	His	Leu	Lys	Ile	Cys	60
				50					55						
Pro	Gln	Gly	Ser	Thr	Cys	Cys	Ser	Gln	Glu	Met	Glu	Glu	Lys	Tyr	75
				65					70						
Ser	Leu	Gln	Ser	Lys	Asp	Asp	Phe	Lys	Ser	Val	Val	Ser	Glu	Gln	90
				80					85						
Cys	Asn	His	Leu	Gln	Ala	Val	Phe	Ala	Ser	Arg	Tyr	Lys	Lys	Phe	105
				95					100						
Asp	Glu	Phe	Phe	Lys	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	120
				110					115						
Asn	Asp	Met	Phe	Val	Lys	Thr	Tyr	Gly	His	Leu	Tyr	Met	Gln	Asn	135
				125					130						
Ser	Glu	Leu	Phe	Lys	Asp	Leu	Phe	Val	Glu	Leu	Lys	Arg	Tyr	Tyr	150
				140					145						
Val	Val	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	165
				155					160						
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Arg	Leu	Val	Asn	Ser	Gln	Tyr	180
				170					175						
His	Phe	Thr	Asp	Glu	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Glu	195
				185					190						
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Leu	Gln	210
				200					205						
Val	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Thr	Phe	Ala	Gln	Gly	Leu	225
				215					220						
Ala	Val	Ala	Gly	Asp	Val	Val	Ser	Lys	Val	Ser	Val	Val	Asn	Pro	240
				230					235						
Thr	Ala	Gln	Cys	Thr	His	Ala	Leu	Leu	Lys	Met	Ile	Tyr	Cys	Ser	255
				245					250						
His	Cys	Arg	Gly	Leu	Val	Thr	Val	Lys	Pro	Cys	Tyr	Asn	Tyr	Cys	270
				260					265						
Ser	Asn	Ile	Met	Arg	Gly	Cys	Leu	Ala	Asn	Gln	Gly	Asp	Leu	Asp	285
				275					280						
Phe	Glu	Trp	Asn	Asn	Phe	Ile	Asp	Ala	Met	Leu	Met	Val	Ala	Glu	300
				290					295						
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	315
				305					310						
Asp	Val	Lys	Ile	Ser	Asp	Ala	Ile	Met	Asn	Met	Gln	Asp	Asn	Ser	330
				320					325						
Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	Cys	Gly	Pro	Pro	Lys	345
				335					340						
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Glu	Ser	Ala	360
				350					355						

350	355	360
Phe Ser Ala Arg	Phe Arg Pro His His	Pro Glu Glu Arg Pro Thr
365	370	375
Thr Ala Ala Gly	Thr Ser Leu Asp Arg	Leu Val Thr Asp Val Lys
380	385	390
Glu Lys Leu Lys	Gln Ala Lys Lys Phe	Trp Ser Ser Leu Pro Ser
395	400	405
Asn Val Cys Asn	Asp Glu Arg Met Ala	Ala Gly Asn Gly Asn Glu
410	415	420
Asp Asp Cys Trp	Asn Gly Lys Gly Lys	Ser Arg Tyr Leu Phe Ala
425	430	435
Val Thr Gly Asn	Gly Leu Ala Asn Gln	Gly Asn Asn Pro Glu Val
440	445	450
Gln Val Asp Thr	Ser Lys Pro Asp Ile	Leu Ile Leu Arg Gln Ile
455	460	465
Met Ala Leu Arg	Val Met Thr Ser Lys	Met Lys Asn Ala Tyr Asn
470	475	480
Gly Asn Asp Val	Asp Phe Phe Asp Ile	Ser Asp Glu Ser Ser Gly
485	490	495
Glu Gly Ser Gly	Ser Gly Cys Glu Tyr	Gln Gln Cys Pro Ser Glu
500	505	510
Phe Asp Tyr Asn	Ala Thr Asp His Ala	Gly Lys Ser Ala Asn Glu
515	520	525
Lys Ala Asp Ser	Ala Gly Val Arg Pro	Gly Ala Gln Ala Tyr Leu
530	535	540
Leu Thr Val Phe	Cys Ile Leu Phe Leu	Val Met Gln Arg Glu Trp
545	550	555

Arg

<210> 161
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 161
 ctccgtggta aacccacag ccc 23

<210> 162
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 162
 tcacatcgat gggatccatg accg 24

 <210> 163
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 163
 ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

 <210> 164
 <211> 870
 <212> DNA
 <213> Homo sapiens

 <400> 164
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 gctgagtgatc ctgacctgag tcatccccag ggcacaggag cctccacgag 100
 ggaacctctoc attatattct tcaagcaact tacagctgca ccgacagttg 150
 cgatgaaagt tctaattctt tccctcctcc tgttgctgcc actaatgctg 200
 atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag 250
 ggaccgaggc caggcttcta ggagatggct ccagggaaggc ggccaagaat 300
 gtgagtgcga agattggttc ctgagagccc cgagaagaaa attcatgaca 350
 gtgtctgggc tgccaaagaa gcagtgcccc tgtgatcatt tcaagggcaa 400
 tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt 450
 ccagagcctg ccagcaattt ctcaaacat gtcagctaag aagctttgct 500
 ctgcctttgt aggagctctg agcgcccact cttccaatta aacattctca 550
 gccaaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc 600
 actctcccac tgtatccacc cctaaatcat tccagtgtct tcaaaaagca 650
 tgtttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700
 cgtcagtcct agcctgtgcc ctccccttac ccaggcttag gcttaattac 750
 ctgaagatt ccaggaaact gtactctcct agctagtgtc atttaacctt 800
 aaatgcaatc aggaagtag caaacagaag tcaataaata tttttaaatg 850
 tcaaaaaaaaa aaaaaaaaaa 870

 <210> 165
 <211> 119
 <212> PRT
 <213> Homo sapiens

 <400> 165
 Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met

1	5	10	15
Leu Met Ser Met	Val Ser Ser Ser	Leu Asn Pro Gly Val Ala	Arg
	20	25	30
Gly His Arg Asp	Arg Gly Gln Ala Ser	Arg Arg Trp Leu Gln	Glu
	35	40	45
Gly Gly Gln Glu	Cys Glu Cys Lys Asp	Trp Phe Leu Arg Ala	Pro
	50	55	60
Arg Arg Lys Phe	Met Thr Val Ser Gly	Leu Pro Lys Lys Gln	Cys
	65	70	75
Pro Cys Asp His	Phe Lys Gly Asn Val	Lys Lys Thr Arg His	Gln
	80	85	90
Arg His His Arg	Lys Pro Asn Lys His	Ser Arg Ala Cys Gln	Glu
	95	100	105
Phe Leu Lys Gln	Cys Gln Leu Arg Ser	Phe Ala Leu Pro Leu	
	110	115	

<210> 166
 <211> 551
 <212> DNA
 <213> Homo sapiens

<400> 166
 aatggctgtc ttagtacttc gctgacagt tgtcctggga ctgcttgtct 50
 tattctgtac ctgctatgca gacgacaaac cagacaagcc agacgacaag 100
 ccagacgact cgggcaaaga cccaaagcca gacttcccca aattcctaag 150
 cctcctgggc acagagatca ttgagaatgc agtcgagttc atcctccgct 200
 ccatgtccag gagcacagga tttatggaat ttgatgataa tgaaggaaaa 250
 cattcatcaa agtgacatcc tcaggacaca cccatgtggc tctgggacaa 300
 tccaagagca gccaaatcct gcttttccag ttggtctcca caagtctctc 350
 aggacagagc cctcaaagca actccaacg agttctcagg attcaggctc 400
 tggcttcaac caaacagaaac tcattttgaa caccctgact gcatttttgc 450
 ttttagaaag ttagaataaa tatggcgctt tgggatcaca tagttgatgg 500
 agaggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550
 a 551

<210> 167
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 167
 Met Ala Val Leu Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu
 1 5 10 15
 Val Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro

	20		25		30
Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe	35	40	45		
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala	50	55	60		
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met	65	70	75		
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys	80	85			

<210> 168
 <211> 1371
 <212> DNA
 <213> Homo sapiens

<400> 168
 ggacgccagc gctgcagag gctgagcagc gaaaaagcca gtgcccagc 50
 ggaagcacag ctccagagctg gtctgccatg gacatcctgg tccactcct 100
 gcagctgctg gtgctgtctt ttaccctgcc cctgcacctg atggctctgc 150
 tgggtgctg gcagcccttg tgcaaaagct acttccccta cctgatggcc 200
 gtgctgactc ccaagagcaa ccgcaaatg gagagcaaga aacgggagct 250
 ctccagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac 300
 tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc 350
 tgcaggggtc cctgcctaga cccaatccc cactttgaga agttcctgac 400
 aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtgggtg 450
 ctctgggaga ggacatgaga cagctggctg atggctccat ggatgtgggtg 500
 gtctgcactc tgggtgctgt ctctgtgcag agcccaagga aggtcctgca 550
 ggaggtcccg agagtactga gaccggggag tgtgctcttt ttctgggagc 600
 atgtggcaga accatatgga agctgggcct tcatgtggga gcaagttttc 650
 gagcccacct ggaacacat tggggatggc tgctgcctca ccagagagac 700
 ctggaaggat ctgagaacg ccagttctc cgaatccaa atggaacgac 750
 agccccctcc ctgaaagtg ctacctgttg ggccccacat catgggaaa 800
 gctgtcaaac aatctttccc aagctccaag gcactcattt gctccttccc 850
 cagctccaa ttagaacaag ccaccacca gcctatctat ctccactga 900
 gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc 950
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 gacagtga aaagctctact tctacgtga ccaggaggg aaacactagg 1050
 accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt 1100

gcctcccaat gttgtccctt tcttcgttc ccatggtaaa gctcctctcg 1150
 ctttctcctt gaggtctacac ccatgcgtct ctaggaactg gtcacaaaag 1200
 tcatggtgcc tgcattccctg ccaagccccc ctgaccctct ctccccacta 1250
 ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg 1300
 atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatatTTTT 1350
 taataaatag acgaaaccac g 1371

<210> 169
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 169
 Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu
 1 5 10 15
 Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro
 20 25 30
 Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro
 35 40 45
 Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser
 50 55 60
 Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu
 65 70 75
 Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro
 80 85 90
 Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys
 95 100 105
 Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu
 110 115 120
 Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp
 125 130 135
 Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val
 140 145 150
 Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg
 155 160 165
 Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr
 170 175 180
 Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp
 185 190 195
 Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys
 200 205 210
 Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln
 215 220 225

Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
 230 235 240
 Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
 245 250 255
 Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
 260 265 270
 Tyr Leu Pro Leu Arg Gly Thr
 275

<210> 170
 <211> 1621
 <212> DNA
 <213> Homo sapiens

<400> 170
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 cctcatcgca ggcagatggt ggggctttgt ccgaacagct ccctctgcc 100
 agcttctgta gataagggtt aaaaactaat atttatatga cagaagaaaa 150
 agatgtcatt ccgtaaaagta aacatcatca tottggtcct ggctgtgtgt 200
 ctcttcttac tggttttgca ccataacttc ctcagcttga gcagtttgtt 250
 aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300
 ttgtcccaaa tgctctcga catgcagtag atgggagaca agaggagatt 350
 cctgtggta tggctgcatc tgaagacagg cttggggggg ccattgcagc 400
 tataaacagc attcagcaca aactcgcct caatgtgatt ttctacattg 450
 ttactotcaa caatacagca gaccatctcc ggtcctgggt caacagtgat 500
 tcctgaaaa gcatcagata caaaattgtc aattttgacc ctaaactttt 550
 ggaaggaaaa gtaaaggagg atcctgacca gggggaatcc atgaaacctt 600
 taacctttgc aaggttctac ttgccaatc tggttcccg cgcagaaga 650
 gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgcctt 700
 ttacaataca gcaactgaagc caggacatgc agctgcattt tcagaagatt 750
 gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtag 800
 aattacattg gctactctga ctataaaaag gaaagaatcc gtaagctttc 850
 catgaaagcc agcacttgct catttaatcc tggagttttt gttgcaaac 900
 tgacggaatg gaaacgacag aatataacta accaactgga aaatggatg 950
 aaactcaatg tagaaggagg actgtatagc agaaccctgg ctggtagcat 1000
 cacacacact cctctgctta tcgtatttta tcaacagcac tctaccatcg 1050
 atcctatgtg gaatgtccgc caccttggtt ccagtgtctg aaaacgatat 1100
 tcacctcagt ttgtaaaaggc tgccaagtta ctccattgga atggacattt 1150

	185		190		195
Phe Ser Glu Asp	Cys Asp Ser Ala Ser Thr Lys Val Val Ile Arg				
	200		205		210
Gly Ala Gly Asn	Gln Tyr Asn Tyr Ile Gly Tyr Leu Asp Tyr Lys				
	215		220		225
Lys Glu Arg Ile	Arg Lys Leu Ser Met Lys Ala Ser Thr Cys Ser				
	230		235		240
Phe Asn Pro Gly	Val Phe Val Ala Asn Leu Thr Glu Trp Lys Arg				
	245		250		255
Gln Asn Ile Thr	Asn Gln Leu Glu Lys Trp Met Lys Leu Asn Val				
	260		265		270
Glu Glu Gly Leu	Tyr Ser Arg Thr Leu Ala Gly Ser Ile Thr Thr				
	275		280		285
Pro Pro Leu Leu	Ile Val Phe Tyr Gln Gln His Ser Thr Ile Asp				
	290		295		300
Pro Met Trp Asn	Val Arg His Leu Gly Ser Ser Ala Gly Lys Arg				
	305		310		315
Tyr Ser Pro Gln	Phe Val Lys Ala Ala Lys Leu Leu His Trp Asn				
	320		325		330
Gly His Leu Lys	Pro Trp Gly Arg Thr Ala Ser Tyr Thr Asp Val				
	335		340		345
Trp Glu Lys Trp	Tyr Ile Pro Asp Pro Thr Gly Lys Phe Asn Leu				
	350		355		360
Ile Arg Arg Tyr	Thr Glu Ile Ser Asn Ile Lys				
	365		370		

<210> 172
 <211> 585
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 71, 76, 86, 91, 162, 220, 269, 281
 <223> unknown base

<400> 172
 tgggtttttgc cccataaatt ccctcagctt gagcagtttg ttaaggaatg 50
 aggttacaga ttccaggaatt nttagncctc aacctntaga ttttgtccca 100
 aatgtttctcc gacatgcagt agatgggaga caagaggaga ttctgtgggt 150
 catcgctgca tntgaagaca ggcttggggg ggccattgca gctataaaca 200
 gcatttcagca caacactcgn tccaatgtga ttttctacat tgttactctc 250
 aacaatacag cagacatnt cgggtcctgg ntcaacagtg attccctgaa 300
 aagcatcaga tacaaaaattg tcaattttga cctaaactt ttggaaggaa 350

aagtaaagga ggatcctgac cagggggaat ccatgaaacc tttaaccttt 400
gcaaggttct acttgccaat tctggttccc agcgcaaaga aggccatata 450
catggatgat gatgtaattg tgcaagtgga tattcttgcc ctttacaata 500
cagcactgaa gccaggacat gcagctgcat tttcagaaga ttgtgatcca 550
gcctctacta aagttgtcat ccgtggagca ggaaa 585

<210> 173
<211> 1866
<212> DNA
<213> Homo sapiens

<400> 173
cgacgctcta gcggttaccg ctgcgggctg gctgggcgta gtggggctgc 50
gcggctgccca cggagctaga gggcaagtgt gctcggccca gcgtgcaggg 100
aacgcgggcg gccagacaac gggctgggct ccggggcctg cggcgcggcg 150
gctgagctgg caggcggggt cggggcgcgg gctgcatccg catctcctcc 200
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<210> 174
 <211> 823
 <212> DNA
 <213> Homo sapiens

<400> 174
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 ctccaccattg aggcagctcc actgtctgtg ctggctctgag ggtgctgcct 150
 gtcattggggg cagccatctc ccaggggggc ctcatcgcca tcgtctgcaa 200
 cggctctctg ggcctcttgc tgctgctgct ctgggtcctc ctctgctggg 250
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ctctaaaaaa aaaaaaaaaa aaa 823

<210> 175

<211> 87

<212> PRT

<213> Homo sapiens

<400> 175

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Asn	Gly	Leu	Val	Gly	Phe	Leu	Leu	Leu	Leu	Leu	Trp	Val	Ile	Leu
				20						25				30

Cys	Trp	Ala	Cys	His	Ser	Arg	Leu	Pro	Thr	Leu	Thr	Leu	Ser	Leu
				35					40					45

Asn	Pro	Val	Pro	Thr	Pro	Ala	Leu	Ala	Pro	Val	Leu	Arg	Arg	Pro
				50					55					60

His	His	Pro	Arg	Ser	Pro	Ala	Met	Lys	Ala	Ala	Thr	Cys	Cys	Ser
				65					70					75

Pro	Glu	Gly	Pro	Trp	Pro	Ser	Leu	Glu	Pro	Arg	Thr
				80					85		

<210> 176

<211> 1660

<212> DNA

<213> Homo sapiens

<400> 176

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atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga 200

gatacaatcc ttggcctgtg tatcctcgca ttagccttgt ctttggccat 250

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aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcacacagg 450

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<210> 177
 <211> 445
 <212> PRT
 <213> Homo sapiens

<400> 177

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Ala	Leu	Ser	Leu	Ala	Met	Met	Phe	Thr	Phe	Arg	Phe	Ile	Thr	Thr
			20						25					30
Leu	Leu	Val	His	Ile	Phe	Ile	Ser	Leu	Val	Ile	Leu	Gly	Leu	Leu
			35						40					45
Phe	Val	Cys	Gly	Val	Leu	Trp	Trp	Leu	Tyr	Tyr	Asp	Tyr	Thr	Asn
			50						55					60
Asp	Leu	Ser	Ile	Glu	Leu	Asp	Thr	Glu	Arg	Glu	Asn	Met	Lys	Cys
			65						70					75
Val	Leu	Gly	Phe	Ala	Ile	Val	Ser	Thr	Gly	Ile	Thr	Ala	Val	Leu
			80						85					90
Leu	Val	Leu	Ile	Phe	Val	Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val

	95		100		105
Glu Leu Phe Gln	Ile Thr Asn Lys Ala	Ile Ser Ser Ala Pro	Phe		
	110		115		120
Leu Leu Phe Gln	Pro Leu Trp Thr Phe	Ala Ile Leu Ile Phe	Phe		
	125		130		135
Trp Val Leu Trp	Val Ala Val Leu Leu	Ser Leu Gly Thr Ala	Gly		
	140		145		150
Ala Ala Gln Val	Met Glu Gly Gly Gln	Val Glu Tyr Lys Pro	Leu		
	155		160		165
Ser Gly Ile Arg	Tyr Met Trp Ser Tyr	His Leu Ile Gly Leu	Ile		
	170		175		180
Trp Thr Ser Glu	Phe Ile Leu Ala Cys	Gln Gln Met Thr Ile	Ala		
	185		190		195
Gly Ala Val Val	Thr Cys Tyr Phe Asn	Arg Ser Lys Asn Asp	Pro		
	200		205		210
Pro Asp His Pro	Ile Leu Ser Ser Leu	Ser Ile Leu Phe Phe	Tyr		
	215		220		225
His Gln Gly Thr	Val Val Lys Gly Ser	Phe Leu Ile Ser Val	Val		
	230		235		240
Arg Ile Pro Arg	Ile Ile Val Met Tyr	Met Gln Asn Ala Leu	Lys		
	245		250		255
Glu Gln Gln His	Gly Ala Leu Ser Arg	Tyr Leu Phe Arg Cys	Cys		
	260		265		270
Tyr Cys Cys Phe	Trp Cys Leu Asp Lys	Tyr Leu Leu His Leu	Asn		
	275		280		285
Gln Asn Ala Tyr	Thr Thr Thr Ala Ile	Asn Gly Thr Asp Phe	Cys		
	290		295		300
Thr Ser Ala Lys	Asp Ala Phe Lys Ile	Leu Ser Lys Asn Ser	Ser		
	305		310		315
His Phe Thr Ser	Ile Asn Cys Phe Gly	Asp Phe Ile Ile Phe	Leu		
	320		325		330
Gly Lys Val Leu	Val Val Cys Phe Thr	Val Phe Gly Gly Leu	Met		
	335		340		345
Ala Phe Asn Tyr	Asn Arg Ala Phe Gln	Val Trp Ala Val Pro	Leu		
	350		355		360
Leu Leu Val Ala	Phe Phe Ala Tyr Leu	Val Ala His Ser Phe	Leu		
	365		370		375
Ser Val Phe Glu	Thr Val Leu Asp Ala	Leu Phe Leu Cys Phe	Ala		
	380		385		390
Val Asp Leu Glu	Thr Asn Asp Gly Ser	Ser Glu Lys Pro Tyr	Phe		
	395		400		405
Met Asp Gln Glu	Phe Leu Ser Phe Val	Lys Arg Ser Asn Lys	Leu		

	410		415		420
Asn Asn Ala Arg Ala Gln Gln Asp Lys His Ser Leu Arg Asn Glu					
	425		430		435
Glu Gly Thr Glu Leu Gln Ala Ile Val Arg					
	440		445		

<210> 178
 <211> 2773
 <212> DNA
 <213> Homo sapiens

<400> 178
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 ttctcactat gaaggcatct gttattgaaa tggtccttgt tttgctgggtg 250
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 gttaactgtg cctcagatca actgcgatgt caaagccgga aagatcatcg 350
 atcctgagtt catttgtaaa tgtccagcag gatgccaaaga ccccaataac 400
 catgtttatg gcactgacgt gtatgcaccc tactccagtg tgtgtggcgc 450
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<210> 179

<211> 678
 <212> PRT
 <213> Homo sapiens

<400> 179

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Phe	Leu	Val	Leu	Leu	Val	Thr	Gly	Val	His	Ser	Asn	Lys	Glu	Thr	
			20						25					30	
Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn	
			35					40						45	
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val	
			50						55					60	
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly	
			65						70					75	
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val	
			80						85					90	
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg	
			95						100					105	
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly	
			110						115					120	
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val	
			125						130					135	
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu	
			140						145					150	
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr	
			155						160					165	
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln	
			170						175					180	
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala	
			185						190					195	
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	
			200						205					210	
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	
			215						220					225	
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	
			230						235					240	
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	
			245						250					255	
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	
			260						265					270	
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	
			275						280					285	
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly	

					290					295					300		
Ser	Thr	Ser	Ile	Gly	305	Lys	Arg	Arg	Phe	Arg	310	Ile	Gln	Lys	Gln	Leu	315
Leu	Ala	Asp	Val	Ala	320	Gln	Ala	Leu	Asp	Ile	325	Gly	Pro	Ala	Gly	Pro	330
Leu	Met	Gly	Val	Val	335	Gln	Tyr	Gly	Asp	Asn	340	Pro	Ala	Thr	His	Phe	345
Asn	Leu	Lys	Thr	His	350	Thr	Asn	Ser	Arg	Asp	355	Leu	Lys	Thr	Ala	Ile	360
Glu	Lys	Ile	Thr	Gln	365	Arg	Gly	Gly	Leu	Ser	370	Asn	Val	Gly	Arg	Ala	375
Ile	Ser	Phe	Val	Thr	380	Lys	Asn	Phe	Phe	Ser	385	Lys	Ala	Asn	Gly	Asn	390
Arg	Ser	Gly	Ala	Pro	395	Asn	Val	Val	Val	Val	400	Met	Val	Asp	Gly	Trp	405
Pro	Thr	Asp	Lys	Val	410	Glu	Glu	Ala	Ser	Arg	415	Leu	Ala	Arg	Glu	Ser	420
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Glu	Lys	Gln	Tyr	Val	440	Val	Glu	Pro	Asn	Phe	445	Ala	Asn	Lys	Ala	Val	450
Cys	Arg	Thr	Asn	Gly	455	Phe	Tyr	Ser	Leu	His	460	Val	Gln	Ser	Trp	Phe	465
Gly	Leu	His	Lys	Thr	470	Leu	Gln	Pro	Leu	Val	475	Lys	Arg	Val	Cys	Asp	480
Thr	Asp	Arg	Leu	Ala	485	Cys	Ser	Lys	Thr	Cys	490	Leu	Asn	Ser	Ala	Asp	495
Ile	Gly	Phe	Val	Ile	500	Asp	Gly	Ser	Ser	Ser	505	Val	Gly	Thr	Gly	Asn	510
Phe	Arg	Thr	Val	Leu	515	Gln	Phe	Val	Thr	Asn	520	Leu	Thr	Lys	Glu	Phe	525
Glu	Ile	Ser	Asp	Thr	530	Asp	Thr	Arg	Ile	Gly	535	Ala	Val	Gln	Tyr	Thr	540
Tyr	Glu	Gln	Arg	Leu	545	Glu	Phe	Gly	Phe	Asp	550	Lys	Tyr	Ser	Ser	Lys	555
Pro	Asp	Ile	Leu	Asn	560	Ala	Ile	Lys	Arg	Val	565	Gly	Tyr	Trp	Ser	Gly	570
Gly	Thr	Ser	Thr	Gly	575	Ala	Ala	Ile	Asn	Phe	580	Ala	Leu	Glu	Gln	Leu	585
Phe	Lys	Lys	Ser	Lys	590	Pro	Asn	Lys	Arg	Lys	595	Leu	Met	Ile	Leu	Ile	600
Thr	Asp	Gly	Arg	Ser		Tyr	Asp	Asp	Val	Arg		Ile	Pro	Ala	Met	Ala	

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<210> 181
 <211> 541
 <212> PRT
 <213> Homo sapiens

<400> 181
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 Asp Pro Ala His Tyr Ser Phe Ser Leu Thr Leu Ile Asp Ala Leu
 35 40 45
 Asp Thr Leu Leu Ile Leu Gly Asn Val Ser Glu Phe Gln Arg Val
 50 55 60
 Val Glu Val Leu Gln Asp Ser Val Asp Phe Asp Ile Asp Val Asn
 65 70 75
 Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu
 80 85 90
 Ser Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala
 95 100 105
 Gly Trp Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala
 110 115 120
 Ala Arg Lys Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro

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Tyr	Gly	Thr	Val	Asn	Leu	Leu	His	Gly	Val	Asn	Pro	Gly	Glu	Thr		
				140					145							150
Pro	Val	Thr	Cys	Thr	Ala	Gly	Ile	Gly	Thr	Phe	Ile	Val	Glu	Phe		
				155					160							165
Ala	Thr	Leu	Ser	Ser	Leu	Thr	Gly	Asp	Pro	Val	Phe	Glu	Asp	Val		
				170					175							180
Ala	Arg	Val	Ala	Leu	Met	Arg	Leu	Trp	Glu	Ser	Arg	Ser	Asp	Ile		
				185					190							195
Gly	Leu	Val	Gly	Asn	His	Ile	Asp	Val	Leu	Thr	Gly	Lys	Trp	Val		
				200					205							210
Ala	Gln	Asp	Ala	Gly	Ile	Gly	Ala	Gly	Val	Asp	Ser	Tyr	Phe	Glu		
				215					220							225
Tyr	Leu	Val	Lys	Gly	Ala	Ile	Leu	Leu	Gln	Asp	Lys	Lys	Leu	Met		
				230					235							240
Ala	Met	Phe	Leu	Glu	Tyr	Asn	Lys	Ala	Ile	Arg	Asn	Tyr	Thr	Arg		
				245					250							255
Phe	Asp	Asp	Trp	Tyr	Leu	Trp	Val	Gln	Met	Tyr	Lys	Gly	Thr	Val		
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Ser	Met	Pro	Val	Phe	Gln	Ser	Leu	Glu	Ala	Tyr	Trp	Pro	Gly	Leu		
				275					280							285
Gln	Ser	Leu	Ile	Gly	Asp	Ile	Asp	Asn	Ala	Met	Arg	Thr	Phe	Leu		
				290					295							300
Asn	Tyr	Tyr	Thr	Val	Trp	Lys	Gln	Phe	Gly	Gly	Leu	Pro	Glu	Phe		
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Tyr	Asn	Ile	Pro	Gln	Gly	Tyr	Thr	Val	Glu	Lys	Arg	Glu	Gly	Tyr		
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Pro	Leu	Arg	Pro	Glu	Leu	Ile	Glu	Ser	Ala	Met	Tyr	Leu	Tyr	Arg		
				335					340							345
Ala	Thr	Gly	Asp	Pro	Thr	Leu	Leu	Glu	Leu	Gly	Arg	Asp	Ala	Val		
				350					355							360
Glu	Ser	Ile	Glu	Lys	Ile	Ser	Lys	Val	Glu	Cys	Gly	Phe	Ala	Thr		
				365					370							375
Ile	Lys	Asp	Leu	Arg	Asp	His	Lys	Leu	Asp	Asn	Arg	Met	Glu	Ser		
				380					385							390
Phe	Phe	Leu	Ala	Glu	Thr	Val	Lys	Tyr	Leu	Tyr	Leu	Leu	Phe	Asp		
				395					400							405
Pro	Thr	Asn	Phe	Ile	His	Asn	Asn	Gly	Ser	Thr	Phe	Asp	Ala	Val		
				410					415							420
Ile	Thr	Pro	Tyr	Gly	Glu	Cys	Ile	Leu	Gly	Ala	Gly	Gly	Tyr	Ile		
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Phe	Asn	Thr	Glu	Ala	His											

NEW! 3-1-1

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<211> 2056
<212> DNA
<213> Homo sapiens
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162

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cactgttcgt	ctggaaaatg	ggccggctgc	tccagtactc	ctgttgcccc	1050
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gtgacctgga	ggaaggtcac	agccacactg	aaaatgggag	gtgcatgaac	1850
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agacagcagg	tgaatgtgat	gtgtgcaatg	cgacgagaat	gcagaagtca	1950
gtaaacatgtg	catgtttgtt	gtgctccttt	tttctgtttg	taaaagtacag	2000
aattcagcaa	ataaaaaggg	ccaccctggc	caaaagcggt	aaaaaaaaaa	2050
aaaaaa	2056				

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<210> 183
<211> 311
<212> PRT
<213> Homo sapiens

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<222> 1-29
<223> Signal peptide

<220>
<221> N-glycosylation sites
<222> 40-43, 134-137
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<223> N-glycosylation sites.

<220>

<221> Tissue factor proteins homology

<222> 92-119

<223> Tissue factor proteins homology

<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

<220>

<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

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				20					25					30	
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser	
				35					40					45	
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	
				50					55					60	
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	
				65					70					75	
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	
				80					85					90	
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	
				95					100					105	
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	
				110					115					120	
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
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Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp
 245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val
 260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
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Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met
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Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
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<210> 184
 <211> 808
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748
 <223> unknown base

<400> 184
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 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200
 ccaaattgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
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 tgacccac 808

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<210> 185
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
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<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
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<210> 187
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
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<210> 188
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 188
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aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150
ctggagaagt acgcgggac ggtgtccctg gtggtgaatg tggccagcga 200
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250
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cacctacagt gtctcattcc coactgttag caagattgca gtcaccggta 400
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cccacctgga acttctgtaa gtacctaga gcccagatg gaaaggtggt 500
aggggcttgg gacccaactg tgtcagtgga ggaggtcaga cccagatca 550
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<210> 189

<211> 187

<212> PRT

<213> Homo sapiens

<400> 189

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Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly	35	40	45	
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Gly	Phe	Thr	50	55	60	
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly	65	70	75	
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly	80	85	90	
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg	95	100	105	
Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val	110	115	120	
Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr	125	130	135	
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala	140	145	150	
Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val				

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<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
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<210> 191
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 191
agtcctgggcc aggtacttga aggc 24

<210> 192
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<213> Artificial Sequence

<220>
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<210> 193
<211> 2187
<212> DNA
<213> Homo sapiens

<400> 193
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260	265	270
Lys Gly Ala Thr Leu Ser His Tyr Asn	Ile Val Asn Asn Ser Asn	
275	280	285
Ile Leu Gly Glu Arg Leu Lys Leu His	Glu Lys Thr Pro Glu Gln	
290	295	300
Leu Arg Met Ile Leu Pro Asn Pro Leu	Tyr His Cys Leu Gly Ser	
305	310	315
Val Ala Gly Thr Met Met Cys Leu Met	Tyr Gly Ala Thr Leu Ile	
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Leu Ala Ser Pro Ile Phe Asn Gly Lys	Lys Ala Leu Glu Ala Ile	
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Ser Arg Glu Arg Gly Thr Phe Leu Tyr	Gly Thr Pro Thr Met Phe	
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Val Asp Ile Leu Asn Gln Pro Asp Phe	Ser Ser Tyr Asp Ile Ser	
365	370	375
Thr Met Cys Gly Gly Val Ile Ala Gly	Ser Pro Ala Pro Pro Glu	
380	385	390
Leu Ile Arg Ala Ile Ile Asn Lys Ile	Asn Met Lys Asp Leu Val	
395	400	405
Val Ala Tyr Gly Thr Thr Glu Asn Ser	Pro Val Thr Phe Ala His	
410	415	420
Phe Pro Glu Asp Thr Val Glu Gln Lys	Ala Glu Ser Val Gly Arg	
425	430	435
Ile Met Pro His Thr Glu Ala Arg Ile	Met Asn Met Glu Ala Gly	
440	445	450
Thr Leu Ala Lys Leu Asn Thr Pro Gly	Glu Leu Cys Ile Arg Gly	
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Tyr Cys Val Met Leu Gly Tyr Trp Gly	Glu Pro Gln Lys Thr Glu	
470	475	480
Glu Ala Val Asp Gln Asp Lys Trp Tyr	Trp Thr Gly Asp Val Ala	
485	490	495
Thr Met Asn Glu Gln Gly Phe Cys Lys	Ile Val Gly Arg Ser Lys	
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Asp Met Ile Ile Arg Gly Gly Glu Asn	Ile Tyr Pro Ala Glu Leu	
515	520	525
Glu Asp Phe Phe His Thr His Pro Lys	Val Gln Glu Val Gln Val	
530	535	540
Val Gly Val Lys Asp Asp Arg Met Gly	Glu Glu Ile Cys Ala Cys	
545	550	555
Ile Arg Leu Lys Asp Gly Glu Glu Thr	Thr Val Glu Glu Ile Lys	

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<210> 197

<211> 346

<212> PRT

<213> Homo sapiens

<400> 197

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Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala		
			20					25						30	
Leu	Glu	Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser	

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Pro Asn Lys Met	Lys Thr Val Lys Cys	Ala 55	Pro Gly Val Asp	Val 60	
Cys Thr Glu Ala	Val Gly Ala Val Glu	Thr 70	Ile His Gly Gln	Phe 75	
Ser Leu Ala Val	Arg Gly Cys Gly Ser	Gly 85	Leu Pro Gly Lys	Asn 90	
Asp Arg Gly Leu	Asp Leu His Gly Leu	Leu 100	Ala Phe Ile Gln	Leu 105	
Gln Gln Cys Ala	Gln Asp Arg Cys Asn	Ala 115	Lys Leu Asn Leu	Thr 120	
Ser Arg Ala Leu	Asp Pro Ala Gly Asn	Glu 130	Ser Ala Tyr Pro	Pro 135	
Asn Gly Val Glu	Cys Tyr Ser Cys Val	Gly 145	Leu Ser Arg Glu	Ala 150	
Cys Gln Gly Thr	Ser Pro Pro Val Val	Ser 160	Cys Tyr Asn Ala	Ser 165	
Asp His Val Tyr	Lys Gly Cys Phe Asp	Gly 175	Asn Val Thr Leu	Thr 180	
Ala Ala Asn Val	Thr Val Ser Leu Pro	Val 190	Arg Gly Cys Val	Gln 195	
Asp Glu Phe Cys	Thr Arg Asp Gly Val	Thr 205	Gly Pro Gly Phe	Thr 210	
Leu Ser Gly Ser	Cys Cys Gln Gly Ser	Arg 220	Cys Asn Ser Asp	Leu 225	
Arg Asn Lys Thr	Tyr Phe Ser Pro Arg	Ile 235	Pro Pro Leu Val	Arg 240	
Leu Pro Pro Pro	Glu Pro Thr Thr Val	Ala 250	Ser Thr Thr Ser	Val 255	
Thr Thr Ser Thr	Ser Ala Pro Val Arg	Pro 265	Thr Ser Thr Thr	Lys 270	
Pro Met Pro Ala	Pro Thr Ser Gln Thr	Pro 280	Arg Gln Gly Val	Glu 285	
His Glu Ala Ser	Arg Asp Glu Glu Pro	Arg 295	Leu Thr Gly Gly	Ala 300	
Ala Gly His Gln	Asp Arg Ser Asn Ser	Gly 310	Gln Tyr Pro Ala	Lys 315	
Gly Gly Pro Gln	Gln Pro His Asn Lys	Gly 325	Cys Val Ala Pro	Thr 330	
Ala Gly Leu Ala	Ala Leu Leu Leu Ala	Val 340	Ala Ala Gly Val	Leu 345	

Leu

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 <211> 1657
 <212> DNA
 <213> Homo sapiens

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 gtctcggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150
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cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

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Val	Leu	His	Ser	Ala	Gln	Gly	Ala	Thr	Leu	Gly	Gly	Pro	Glu	Ala
				20					25					30
Glu	Ser	Thr	Ile	Glu	Asn	Tyr	Ala	Ser	Arg	Pro	Glu	Ala	Phe	Asn
				35					40					45
Thr	Pro	Phe	Leu	Asn	Ile	Asp	Lys	Leu	Arg	Ser	Ala	Phe	Lys	Ala
				50					55					60
Asp	Glu	Phe	Leu	Asn	Trp	His	Ala	Leu	Phe	Glu	Ser	Ile	Lys	Arg
				65					70					75
Lys	Leu	Pro	Phe	Leu	Asn	Trp	Asp	Ala	Phe	Pro	Lys	Leu	Lys	Gly
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Leu	Arg	Ser	Ala	Thr	Pro	Asp	Ala	Gln						
				95										

<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

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atgatttaaat aaccatcctt tgcaagttt tatgaggctt taggggaatg 300
tcaacctca aatttttggt atactagatg gcttccattt acccaccact 350
attttaagggt ccttttattt ttagggtcaa gggtcatttg acttgagaaa 400
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cctgggtgcc cctgacacat ttatgtagtg atccacaaa tgtgattggt 550
aatttaaatg ttatttctaatt attagtacat tcaagttgtga tgtaatatga 600
ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650
atttgtagat aaagactgaa tagtgatg 678

<210> 203
 <211> 52
 <212> PRT
 <213> Homo sapiens

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 Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser
 35 40 45
 Cys Gly Phe Ala Gly His Ser
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<210> 204
 <211> 1917
 <212> DNA
 <213> Homo sapiens

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 tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200
 tgggtgcata gaagaggatc taactccttt ccgaggagcg atctccagga 250
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 actaagaaca gactgtaccg ggaaaatgac tgcattgttc cctcaagggtg 350
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<210> 205
 <211> 392
 <212> PRT
 <213> Homo sapiens

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 Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn
 35 40 45
 Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val
 50 55 60
 Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys
 65 70 75
 Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln
 80 85 90
 Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

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180

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0936331203

<210> 207
 <211> 262
 <212> PRT
 <213> Homo sapiens

<400> 207
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 20 25 30
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 35 40 45
 Ala Arg Gln Gly Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu
 50 55 60
 Ala Pro Leu Ala Trp Asp Leu Gly Leu Leu Leu Phe Val Gly
 65 70 75
 Gln His Ser Leu Met Ala Ala Glu Arg Val Lys Ala Trp Thr Ser
 80 85 90
 Arg Tyr Phe Gly Val Leu Gln Arg Ser Leu Tyr Val Ala Cys Thr
 95 100 105
 Ala Leu Ala Leu Gln Leu Val Met Arg Tyr Trp Glu Pro Ile Pro
 110 115 120
 Lys Gly Pro Val Leu Trp Glu Ala Arg Ala Glu Pro Trp Ala Thr
 125 130 135
 Trp Val Pro Leu Leu Cys Phe Val Leu His Val Ile Ser Trp Leu
 140 145 150
 Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr Ala Glu Leu Met
 155 160 165
 Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu Gly Glu Pro
 170 175 180
 Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser His Leu
 185 190 195
 Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val Val
 200 205 210
 Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
 215 220 225
 Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg
 230 235 240
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 245 250 255
 Pro Gln Asp Gly Glu Ala Glu
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<210> 208
 <211> 2095
 <212> DNA

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Val Thr Glu Phe Cys Pro Asn Ala Lys Tyr Val Met Lys Thr Asp
170 175 180

Thr Asp Val Phe Ile Asn Thr Gly Asn Leu Val Lys Tyr Leu Leu
185 190 195

Asn Leu Asn His Ser Glu Lys Phe Phe Thr Gly Tyr Pro Leu Ile
200 205 210

Asp Asn Tyr Ser Tyr Arg Gly Phe Tyr Gln Lys Thr His Ile Ser
215 220 225

Tyr Gln Glu Tyr Pro Phe Lys Val Phe Pro Pro Tyr Cys Ser Gly
230 235 240

Leu Gly Tyr Ile Met Ser Arg Asp Leu Val Pro Arg Ile Tyr Glu
245 250 255

Met Met Gly His Val Lys Pro Ile Lys Phe Glu Asp Val Tyr Val
260 265 270

Gly Ile Cys Leu Asn Leu Leu Lys Val Asn Ile His Ile Pro Glu
275 280 285

Asp Thr Asn Leu Phe Phe Leu Tyr Arg Ile His Leu Asp Val Cys
290 295 300

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Ile Ile Thr Phe Trp Gln Val Met Leu Arg Asn Thr Thr Cys His
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Tyr

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<211> 745
<212> DNA
<213> Homo sapiens

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<210> 211
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 211
 Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu
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 Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn
 20 25 30
 Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu
 35 40 45
 His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp
 50 55 60
 Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu
 65 70 75
 Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val
 80 85 90
 Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys
 95 100 105
 Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Lys Gly Leu Met
 110 115 120
 Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly
 125 130 135
 Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala
 140 145 150
 Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys
 155 160 165
 Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly
 170 175 180
 Asp Thr Val Glu Asn
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<210> 212
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 212
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aaaagt 1706

<210> 213

<211> 299

<212> FRT

<213> Homo sapiens

<400> 213

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				20					25					30
Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly
				35					40					45
Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg
				50					55					60
Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu
				65					70					75
Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala
				80					85					90
Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly
				95					100					105
Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys
				110					115					120
Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys
				125					130					135
Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn
				140					145					150
Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala
				155					160					165
Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr
				170					175					180
Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr
				185					190					195
Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro
				200					205					210
Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His
				215					220					225
Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg
				230					235					240
Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser
				245					250					255
Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp
				260					265					270
Arg	Arg	Glu	Arg	Ser	Arg	Ser	Phe	Glu	Arg	Ser	His	Lys	Ser	Lys

275

280

285

His His Gly Gly Ser Arg Ser Gly His Gly Arg His Arg Arg
290 295

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<210> 214
<211> 730
<212> DNA
<213> Homo sapiens
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<220>
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<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663
<223> unknown base
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gcattgcttt ttacagaaat atattanctt tttagagtaa ttctagttt 150
ggatttgtaat atgaaattat ttaaaagggc ttcgctcata tataggaaaa 200
tcgcatatgg tcctagtatt aaattnttat tgcttactga tttttttgag 250
ttaagagttg ttatatgnta gaatatgagg atgtgaatat aaataagaga 300
agaaaaaaga ataaagtaga ttgagctccc aattttatgt aagcttcaga 350
agaactgggt tgtttacatg caagcttata gttgaaatat tttcaggaa 400
ttacatgaat gacagctctc gaaccaatgt gtttgttoga tttaaccag 450
agantatagc atgtgcttgc atctaccttg cagntagagc acttcagatt 500
cogttgccaa ctngtcccca ttggtttcct ctttttggtg ctacagaaga 550
ggaaatccag gaaatntgca tagaacaact taggctttat accagaaaaa 600
agccaaacta tgaattactg gaaaagaag tagaaaaag aaaagtagcc 650
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agccctttca accotgggtg gattttctcc 730

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<210> 215
<211> 1807
<212> DNA
<213> Homo sapiens
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caccctcat gcacaggctg gcgcccaact gctcttcgc gcgctggctg 150
ctctgtaacg gcaagtttgtt cggatacaag caccctctgc aggaggagct 200
tcgggcctcg gcgggggaagc cgaggccgac aggcaggaaa gagcgggtggg 250
ccaatgcctc taagtgaagag aagccactat ctgtcccgcg agatgcccg 300
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 gcgtgtacct cttcacagag gctactact acatgctggg accagccaag 450
 gagactaaca ttgctgtgtt ctggtgcctg ctcacggtga ccttctccat 500
 caagatgttc ctgacagtga cacggctgta cttcagcgcc gaggaggggg 550
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 gcagtgtgtg gctctgtgct ggggtgcctc ctcaccttcc caggcctgcg 800
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<210> 216

<211> 479
 <212> PRT
 <213> Homo sapiens

<400> 216

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Thr	Leu	Met	His	Arg	Leu	Ala	Pro	His	Cys	Ser	Phe	Ala	Arg	Trp	
				20					25					30	
Leu	Leu	Cys	Asn	Gly	Ser	Leu	Phe	Arg	Tyr	Lys	His	Pro	Ser	Glu	
				35					40					45	
Glu	Glu	Leu	Arg	Ala	Leu	Ala	Gly	Lys	Pro	Arg	Pro	Arg	Gly	Arg	
				50					55					60	
Lys	Glu	Arg	Trp	Ala	Asn	Gly	Leu	Ser	Glu	Glu	Lys	Pro	Leu	Ser	
				65					70					75	
Val	Pro	Arg	Asp	Ala	Pro	Phe	Gln	Leu	Glu	Thr	Cys	Pro	Leu	Thr	
				80					85					90	
Thr	Val	Asp	Ala	Leu	Val	Leu	Arg	Phe	Phe	Leu	Glu	Tyr	Gln	Trp	
				95					100					105	
Phe	Val	Asp	Phe	Ala	Val	Tyr	Ser	Gly	Gly	Val	Tyr	Leu	Phe	Thr	
				110					115					120	
Glu	Ala	Tyr	Tyr	Tyr	Met	Leu	Gly	Pro	Ala	Lys	Glu	Thr	Asn	Ile	
				125					130					135	
Ala	Val	Phe	Trp	Cys	Leu	Leu	Thr	Val	Thr	Phe	Ser	Ile	Lys	Met	
				140					145					150	
Phe	Leu	Thr	Val	Thr	Arg	Leu	Tyr	Phe	Ser	Ala	Glu	Glu	Gly	Gly	
				155					160					165	
Glu	Arg	Ser	Val	Cys	Leu	Thr	Phe	Ala	Phe	Leu	Phe	Leu	Leu	Leu	
				170					175					180	
Ala	Met	Leu	Val	Gln	Val	Val	Arg	Glu	Glu	Thr	Leu	Glu	Leu	Gly	
				185					190					195	
Leu	Glu	Pro	Gly	Leu	Ala	Ser	Met	Thr	Gln	Asn	Leu	Glu	Pro	Leu	
				200					205					210	
Leu	Lys	Lys	Gln	Gly	Trp	Asp	Trp	Ala	Leu	Pro	Val	Ala	Lys	Leu	
				215					220					225	
Ala	Ile	Arg	Val	Gly	Leu	Ala	Val	Val	Gly	Ser	Val	Leu	Gly	Ala	
				230					235					240	
Phe	Leu	Thr	Phe	Pro	Gly	Leu	Arg	Leu	Ala	Gln	Thr	His	Arg	Asp	
				245					250					255	
Ala	Leu	Thr	Met	Ser	Glu	Asp	Arg	Pro	Met	Leu	Gln	Phe	Leu	Leu	
				260					265					270	
His	Thr	Ser	Phe	Leu	Ser	Pro	Leu	Phe	Ile	Leu	Trp	Leu	Trp	Thr	
				275					280					285	
Lys	Pro	Ile	Ala	Arg	Asp	Phe	Leu	His	Gln	Pro	Pro	Phe	Gly	Glu	

	290		295		300
Thr Arg Phe Ser	Leu Leu Ser Asp Ser	Ala Phe Asp Ser Gly Arg			
	305		310		315
Leu Trp Leu Leu	Val Val Leu Cys Leu	Leu Arg Leu Ala Val Thr			
	320		325		330
Arg Pro His Leu	Gln Ala Tyr Leu Cys	Leu Ala Lys Ala Arg Val			
	335		340		345
Glu Gln Leu Arg	Arg Glu Ala Gly Arg	Ile Glu Ala Arg Glu Ile			
	350		355		360
Gln Gln Arg Val	Val Arg Val Tyr Cys	Tyr Val Thr Val Val Ser			
	365		370		375
Leu Gln Tyr Leu	Thr Pro Leu Ile Leu	Thr Leu Asn Cys Thr Leu			
	380		385		390
Leu Leu Lys Thr	Leu Gly Gly Tyr Ser	Trp Gly Leu Gly Pro Ala			
	395		400		405
Pro Leu Leu Ser	Pro Asp Pro Ser Ser	Ala Ser Ala Ala Pro Ile			
	410		415		420
Gly Ser Gly Glu	Asp Glu Val Gln Gln	Thr Ala Ala Arg Ile Ala			
	425		430		435
Gly Ala Leu Gly	Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly Val			
	440		445		450
Leu Ala Tyr Leu	Ile Trp Trp Thr Ala	Ala Cys Gln Leu Leu Ala			
	455		460		465
Ser Leu Phe Gly	Leu Tyr Phe His Gln	His Leu Ala Gly Ser			
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<210> 217
 <211> 574
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 5, 146
 <223> unknown base

<400> 217
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 ctgctggcca tgctggtgca agcg 574
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 <211> 2571
 <212> DNA
 <213> Homo sapiens
 <400> 218
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<210> 219
<211> 632
<212> PRT
<213> Homo sapiens

<400> 219
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Leu Cys Lys Gly	Ala Ser His Tyr Gly	Leu Thr Lys Asp Arg	Lys
35	40		45
Arg Arg Ser Gln	Asp Gly Cys Pro Asp	Gly Cys Ala Ser Leu	Thr
50	55		60
Ala Thr Ala Pro	Ser Pro Glu Val Ser	Ala Ala Thr Ile	Ser
65	70		75
Leu Met Thr Asp	Glu Pro Gly Leu Asp	Asn Pro Ala Tyr Val	Ser
80	85		90
Ser Ala Glu Asp	Gly Gln Pro Ala Ile	Ser Pro Val Asp Ser	Gly
95	100		105
Arg Ser Asn Arg	Thr Arg Ala Arg Pro	Phe Glu Arg Ser Thr	Ile
110	115		120
Arg Ser Arg Ser	Phe Lys Lys Ile Asn	Arg Ala Leu Ser Val	Leu
125	130		135
Arg Arg Thr Lys	Ser Gly Ser Ala Val	Ala Asn His Ala Asp	Gln
140	145		150
Gly Arg Glu Asn	Ser Glu Asn Thr Thr	Ala Pro Glu Val Phe	Pro
155	160		165
Arg Leu Tyr His	Leu Ile Pro Asp Gly	Glu Ile Thr Ser Ile	Lys
170	175		180
Ile Asn Arg Val	Asp Pro Ser Glu Ser	Leu Ser Ile Arg Leu	Val
185	190		195
Gly Gly Ser Glu	Thr Pro Leu Val His	Ile Ile Gln His	Ile
200	205		210
Tyr Arg Asp Gly	Val Ile Ala Arg Asp	Gly Arg Leu Leu Pro	Gly
215	220		225
Asp Ile Ile Leu	Lys Val Asn Gly Met	Asp Ile Ser Asn Val	Pro
230	235		240
His Asn Tyr Ala	Val Arg Leu Leu Arg	Gln Pro Cys Gln Val	Leu
245	250		255
Trp Leu Thr Val	Met Arg Glu Gln Lys	Phe Arg Ser Arg Asn	Asn
260	265		270
Gly Gln Ala Pro	Asp Ala Tyr Arg Pro	Arg Asp Asp Ser Phe	His
275	280		285
Val Ile Leu Asn	Lys Ser Ser Pro Glu	Glu Gln Leu Gly Ile	Lys
290	295		300
Leu Val Arg Lys	Val Asp Glu Pro Gly	Val Phe Ile Phe Asn	Val
305	310		315
Leu Asp Gly Gly	Val Ala Tyr Arg His	Gly Gln Leu Glu Glu	Asn

[illegible]

<210> 220
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 220
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 aggatagaag ctgcacaggg cagctttact tactccagca ccttccctctc 100
 ccaggcaaat ggtgctgacc atcttttgga tacaatctca tggatacgag 150
 gtttttaaca toatcagccc aagcaacaat ggtggcaatg ttcaggagac 200
 agtgacaatt gataatgaaa aaaataccgc catcgttaac atccatgcag 250
 gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300
 tccagggtgc tctccgaag agcctgcttt atcctgaaga tggaccatca 350
 gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400
 ctctggacaa catgttctcc aacaaatata cctgggtcaa gtacaacctt 450
 ctggagctct tgatcaaaga cgtggattgg ttctgtcttg ggtcacccat 500
 tgagaaactc tgcaaacata tccctttgta taagggggaa gtggttgaaa 550
 acacacataa tgtcgtgtgt ggaggctgtg caaaggctgg gtcctctggc 600
 atcttgggaa ttccaatctg tgcagacatt catgtttagg atgattagcc 650
 ctctgtgttt atcttttcaa agaaatacat ccttggttta cactcaaaag 700
 tcaaatataa ttctttccca atgcccacac taattttgag attcagtcag 750
 aaaatataaa tgctgtattt ata 773

<210> 221
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Lys Ile Leu Val Ala Phe Leu Val Val Leu Thr Ile Phe Gly
 1 5 10 15
 Ile Gln Ser His Gly Tyr Glu Val Phe Asn Ile Ile Ser Pro Ser
 20 25 30
 Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu
 35 40 45
 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
 50 55 60
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
 65 70 75
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
 80 85 90

Ile Pro Pro Leu Asn Asn Leu Gln Trp Tyr Ile Tyr Glu Lys Gln
 95 100 105
 Ala Leu Asp Asn Met Phe Ser Asn Lys Tyr Thr Trp Val Lys Tyr
 110 115 120
 Asn Pro Leu Glu Ser Leu Ile Lys Asp Val Asp Trp Phe Leu Leu
 125 130 135
 Gly Ser Pro Ile Glu Lys Leu Cys Lys His Ile Pro Leu Tyr Lys
 140 145 150
 Gly Glu Val Val Glu Asn Thr His Asn Val Gly Ala Gly Gly Cys
 155 160 165
 Ala Lys Ala Gly Leu Leu Gly Ile Leu Gly Ile Ser Ile Cys Ala
 170 175 180
 Asp Ile His Val

<210> 222
 <211> 992
 <212> DNA
 <213> Homo sapiens

<400> 222
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 acccaccgag gcatggggct ccttgggtgt ttctgtctgg ccgtgtctgg 100
 tgccagcagc ttctccaagg caccggagga agaaattacc cctgtgtgtc 150
 ccattgccta caaagtctct gaagttttcc ccaaaggcgc ctgggtgtct 200
 ataacctgct gtgcacccca gccaccaccc cccatcacct attccctctg 250
 tggaaaccaag aacatcaagg tggccaagaa ggtggtgaag acccagcagc 300
 cggcctctct caacctcaac gtcacactca agtccagtc agacctgtct 350
 acctactctt gccgggggtc ctccacctca ggtgcccatg tggacagtgc 400
 caggctacag atgcaactgg agctgtgtgt caagccagtgt tctgagctgc 450
 gggccaactt cactctgcag gacagagggg caggcccccag ggtggagatg 500
 atctgccagg cgtctctggg cagccacact atcaccaaca gcctgatcgg 550
 gaaggatggg cagggtccacc tgcagcagag accatgccac aggcagcctg 600
 ccaacttctc ctctctgcgc agccagacat cggactgggt ctggtgccag 650
 gctgcaaaca acgccaatgt ccagcacagc gccctcacag tgggtccccc 700
 aggtggtgac cagaagatgg aggactggca ggggtccctg gagagcccca 750
 tccttgctct gccgtctcac aggcagcccc gccgtctgag tgaagaggag 800
 ttgtgggggt tcaggatagg gaatggggag gtcagaggac gcaaagcagc 850
 agccatgtag aatgaaccgt ccagagagcc aagcacggca gaggactgca 900

ggccatcagc gtgcactgtt cgtatttgga gttcatgcaa aatgagtgtg 950

ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223

<211> 265

<212> PRT

<213> Homo sapiens

<400> 223

Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser
1 5 10 15

Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser
20 25 30

Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val
35 40 45

Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr
50 55 60

Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val
65 70 75

Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu Lys
80 85 90

Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr
95 100 105

Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu
110 115 120

Leu Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu
125 130 135

Gln Asp Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala
140 145 150

Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp
155 160 165

Gly Gln Val His Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala
170 175 180

Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys
185 190 195

Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu Thr Val
200 205 210

Val Pro Pro Gly Gly Asp Gln Lys Met Glu Asp Trp Gln Gly Pro
215 220 225

Leu Glu Ser Pro Ile Leu Ala Leu Pro Leu Tyr Arg Ser Thr Arg
230 235 240

Arg Leu Ser Glu Glu Glu Phe Gly Gly Phe Arg Ile Gly Asn Gly
245 250 255

Glu Val Arg Gly Arg Lys Ala Ala Ala Met
260 265

<210> 224
 <211> 1297
 <212> DNA
 <213> Homo sapiens

<400> 224
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 cttctgtctcc tgcgtgccgg ctggtcccg gctgggcgag ccgaccctca 100
 ctctctttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150
 ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttactat 200
 gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250
 aaatgtcaca acggcctgga aagcacagaa ccagtagctg agagaggtgg 300
 tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350
 cccaaggaa cctcacccct gcaggcaagg atgtcttgtg agcagaaaag 400
 tgaaggacac agcagtggat cttggcagtt cagtttcgat ggcagatct 450
 tctctctctt tgactcagag aagagaatgt ggacaacggt tcatctgga 500
 gccagaaaaga tgaagaaaaa gtggggagaat gacaagggtg tggccatgtc 550
 ctccattac ttctcaatgg gagactgtat aggatggctt gaggaactct 600
 tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accactcgcc 650
 atgtcctcag gcacaacca actcagggcc acagccacca cctcatcct 700
 ttgtgcctc ctcctcatcc tcccctgctt catcctcctt ggcactctgag 750
 gagagtccct tagagtgaca ggttaaagct gataccaaaa ggctcctgtg 800
 agcacggtct tgatcaaaact cgccttctg tctggccagc tgcccacgac 850
 ctacggtgta tgtccagtgg cctccagcag atcatgatga catcatggac 900
 ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950
 agttatacct aacatattat gcaattttct cttggtgcta cctgatggaa 1000
 ttctgcact taaagtctg gctgactaaa caagatatat cattttcttt 1050
 cttctctttt tgtttggaaa atcaagtact tctttgaatg atgatctctt 1100
 tcttgcaaat gatattgtca gtaaaataat cactgttagac ttcagacctc 1150
 tggggattct ttccgtgtcc tgaaagagaa tttttaaatt atttaataag 1200
 aaaaaattta tattaatgat tgtttccttt agtaatttat tgttctgtac 1250
 tgatatattaa ataaagagtt ctatttccca aaaaaaaaaa aaaaaaa 1297

<210> 225
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 225

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Met Ala Ala Ala Ala Thr Lys Ile Leu Leu Cys Leu Pro Leu
 1          5          10          15

Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
 20          25          30

His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
 35          40          45

Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
 50          55          60

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
 65          70          75

Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
 80          85          90

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
 95          100          105

Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
 110          115          120

Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
 125          130          135

Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
 140          145          150

Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
 155          160          165

Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
 170          175          180

Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
 185          190          195

Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
 200          205          210

Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
 215          220          225

Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
 230          235          240

Phe Ile Leu Pro Gly Ile
 245

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<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

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gggaaagcca ttctgaaaac ccattctatac aaactatata ttttcatttc 50

tgctgctagc tgcttgggc ctcacaattt tcattctgtt ttctgacttt 100

caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

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ggttttaatt ttggtggttag cccctaccca attctggtgt ggctttcttt 200
 gcagaggatt ccacottcaa aatcatgaac tctggctgtt gatcaaaaga 250
 gaatttggtat tctactctaa aagtcaatat aggacttggc aaaagaagct 300
 agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350
 atggcaaaaa tggattctac atcaacggag gctatgaaag ccatgaacag 400
 attcaaaaaa gaaaactcaa attgggaggc caaccacag aacagcattt 450
 ctggggccagg ctgtaatcag aattgtgtgc gtacatgtgc aacagcattg 500
 cttttttccc caaaattaac acattgtgga gaagtgtatga tactctcccc 550
 ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600
 aaaccttgca gcaagggacc ttagataggg ttattctgac tgtatgcttt 650
 accaatgaga gaaaaaaatg catttctgtg atcatccttt tcaataaact 700
 gtattcattt tgaaaaaaa aaaaaaaaaa aaaaa 735

<210> 227
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 227
 Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu
 1 5 10 15
 Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly
 20 25 30
 Phe His Leu Gln Asn His Glu Leu Trp Leu Ile Lys Arg Glu
 35 40 45
 Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys
 50 55 60
 Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr
 65 70 75
 Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu
 80 85 90
 Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln
 95 100 105
 Pro Thr Glu Gln His Phe Trp Ala Arg Leu
 110 115

<210> 228
 <211> 2185
 <212> DNA
 <213> Homo sapiens

<400> 228
 gttctccttt ccgagccaaa atcccaggcg atgggtgaatt atgaacgtgc 50
 cacaccatga agctcttctg gcaggtaact gtgcaccacc acaccttgaa 100

tgccatcctg ctcccgttcg tctacctcac ggcgcaagtg tggattctgt 150
 gtgcagccat cgctgctgcc gctcagccg ggccccagaa ctgcccctcc 200
 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgcggggg 250
 cctctccgag gtcccgaggt gtattcctc gaacaccccg tacctcaacc 300
 tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350
 caccacctgg aggtcctgca gttgggcagg aactccatcc ggcagattga 400
 ggtggggggc ttcaacggcc tggccagcct caacacccgt gagctgttcg 450
 acaactggct gacagtcctc cctagcgggg cctttgaata cctgtccaag 500
 ctgccccgag tctggtctcg caacaacccc atcgaaagca tcccccttta 550
 cgcttcaac cgggtgccct cctcatcgcg cctggacttg ggggagctca 600
 agaagctgga gtatatctct gagggagctt ttgaggggct gtccaacctc 650
 aagtatctga acttgggcat gtgcaacatt aaagacatgc ccaatctcac 700
 cccctggtg gggctggagg agctggagat gtcagggaac cacttccctg 750
 agatcaggcc tggctccttc catggcctga gctccctcaa gaagctctgg 800
 gtcataact cacaggtcag cctgattgag cggaatgctt ttgacgggct 850
 ggcttcaact gtggaactca acttggccca caataacctc tcttctttgc 900
 cccatgaact ctttaccccg ctgaggtagc tgggtggagt gcactctaac 950
 cacaacctt ggaactgtga ttgtgacatt ctgtggctag cctggtggct 1000
 tcgagagtat ataccacca attccaactg ctgtggccgc tgtcatgtct 1050
 ccattgcaat gcgaggccgc tacctcgttg aggtggacca ggcctccttc 1100
 cagtgtcttg ccccttctat catggagcca cctcgagacc tcaacatttc 1150
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 tccaactaca gcttcttcac cacagtaaca gtggagacca cggagatctc 1450
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aaacttcgta agcggcacca gcagcggagt acagtcacag ccgcccggac 1750
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 cagcaacagc agctccgtcc ggtgtatcag gtgagggggc agtagtgctg 1850
 cccacaattc atgaccatat taactacaac acctacaac cagcacatgg 1900
 ggcccactgg acagaaaaca gcttggggaa ctctctgcac cccacagtca 1950
 ccactatctc tgaaccttat ataattcaga ccataccaa ggacaaggta 2000
 caggaaaactc aaatatgact cccctcccc aaaaaactta taaatgcaa 2050
 tagaatgcac acaaagacag caacttttgt acagagtggtg gagagacttt 2100
 ttctgtgata tgcttatata ttaagtctat gggctggtta aaaaaaacg 2150
 attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229
 <211> 653
 <212> PRT
 <213> Homo sapiens

<400> 229
 Met Lys Leu Leu Trp Gln Val Thr Val His His His Thr Trp Asn
 1 5 10
 Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile
 20 25 30
 Leu Cys Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn
 35 40 45
 Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val
 50 55 60
 Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser
 65 70 75
 Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile
 80 85 90
 Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln
 95 100 105
 Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn
 110 115 120
 Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu
 125 130 135
 Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg
 140 145 150
 Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
 155 160 165
 Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu
 170 175 180
 Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu

185	190	195
Phe Asn Leu Lys Tyr Leu Asn Leu Gly Met Cys Asn Ile Lys Asp		
200	205	210
Met Pro Asn Leu Thr Pro Leu Val Gly Leu Glu Glu Leu Glu Met		
215	220	225
Ser Gly Asn His Phe Pro Glu Ile Arg Pro Gly Ser Phe His Gly		
230	235	240
Leu Ser Ser Leu Lys Lys Leu Trp Val Met Asn Ser Gln Val Ser		
245	250	255
Leu Ile Glu Arg Asn Ala Phe Asp Gly Leu Ala Ser Leu Val Glu		
260	265	270
Leu Asn Leu Ala His Asn Asn Leu Ser Ser Leu Pro His Asp Leu		
275	280	285
Phe Thr Pro Leu Arg Tyr Leu Val Glu Leu His Leu His His Asn		
290	295	300
Pro Trp Asn Cys Asp Cys Asp Ile Leu Trp Leu Ala Trp Trp Leu		
305	310	315
Arg Glu Tyr Ile Pro Thr Asn Ser Thr Cys Cys Gly Arg Cys His		
320	325	330
Ala Pro Met His Met Arg Gly Arg Tyr Leu Val Glu Val Asp Gln		
335	340	345
Ala Ser Phe Gln Cys Ser Ala Pro Phe Ile Met Asp Ala Pro Arg		
350	355	360
Asp Leu Asn Ile Ser Glu Gly Arg Met Ala Glu Leu Lys Cys Arg		
365	370	375
Thr Pro Pro Met Ser Ser Val Lys Trp Leu Leu Pro Asn Gly Thr		
380	385	390
Val Leu Ser His Ala Ser Arg His Pro Arg Ile Ser Val Leu Asn		
395	400	405
Asp Gly Thr Leu Asn Phe Ser His Val Leu Leu Ser Asp Thr Gly		
410	415	420
Val Tyr Thr Cys Met Val Thr Asn Val Ala Gly Asn Ser Asn Ala		
425	430	435
Ser Ala Tyr Leu Asn Val Ser Thr Ala Glu Leu Asn Thr Ser Asn		
440	445	450
Tyr Ser Phe Phe Thr Thr Val Thr Val Glu Thr Thr Glu Ile Ser		
455	460	465
Pro Glu Asp Thr Thr Arg Lys Tyr Lys Pro Val Pro Thr Thr Ser		
470	475	480
Thr Gly Tyr Gln Pro Ala Tyr Thr Thr Ser Thr Thr Val Leu Ile		
485	490	495
Gln Thr Thr Arg Val Pro Lys Gln Val Ala Val Pro Ala Thr Asp		

	500		505		510
Thr Thr Asp Lys	Met Gln Thr Ser Leu Asp Glu Val Met Lys Thr				
	515		520		525
Thr Lys Ile Ile	Ile Gly Cys Phe Val Ala Val Thr Leu Leu Ala				
	530		535		540
Ala Ala Met Leu	Ile Val Phe Tyr Lys Leu Arg Lys Arg His Gln				
	545		550		555
Gln Arg Ser Thr	Val Thr Ala Ala Arg Thr Val Glu Ile Ile Gln				
	560		565		570
Val Asp Glu Asp	Ile Pro Ala Ala Thr Ser Ala Ala Ala Thr Ala				
	575		580		585
Ala Pro Ser Gly	Val Ser Gly Glu Gly Ala Val Val Leu Pro Thr				
	590		595		600
Ile His Asp His	Ile Asn Tyr Asn Thr Tyr Lys Pro Ala His Gly				
	605		610		615
Ala His Trp Thr	Glu Asn Ser Leu Gly Asn Ser Leu His Pro Thr				
	620		625		630
Val Thr Thr Ile	Ser Glu Pro Tyr Ile Ile Gln Thr His Thr Lys				
	635		640		645
Asp Lys Val Gln	Glu Thr Gln Ile				
	650				

<210> 230
 <211> 2846
 <212> DNA
 <213> Homo sapiens

<400> 230
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 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150
 tcgggagtgct tgtgaatatg atcagattga gtgcgtctgc ccoggaaaga 200
 gggaagtogt ggggtataacc atcccttgct gcaggaatga ggagaatgag 250
 tgtgactcct gctgatccca cccaggttgt accatctttg aaaactgcaa 300
 gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450
 aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500
 ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600
 ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

gcataaggatc ctactccac gtctcttcc actccgatgg ctccaagaat 700
 tttagcggtt tccatgccat ttatgaggag atcacagcat gctctcato 750
 cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggatcttaca 800
 agtgtgcctg cttggcaggc tatactgggc agcgctgtga aaatctcctt 850
 gaagaaagaa actgctcaga cctggggggc ccagtcaatg ggtaccagaa 900
 aataacaggg ggcctgggc ttatcaacgg acgccatgct aaaattggca 950
 cctgtgtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag 1000
 aaaagaactt gccagcagaa tggagagtgg tcagggaaaac agcccatctg 1050
 cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag 1100
 ttcttcgat gcaggttcag tcaagggaga caccattaca ccagctatac 1150
 tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc 1200
 agcccttccc ttggagatc tgcccatggg ataccaacat ctgcataccc 1250
 agctccagta tgagtgcac tcaccttct accgccgcct gggcagcagc 1300
 aggaggacat gtctgaggac tgggaagtgg agtggggggg caccatcctg 1350
 catccctatc tcgggaaaa ttgagaacat cactgctcca aagaccaag 1400
 ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg 1450
 catgacggca gcctacaaa gggagcgtgg ttctagtct gcagcgggtc 1500
 cctggtgaat gagcgcactg tgggtgtggc tgccactgt gttactgacc 1550
 tggggaaggt caccatgac aagacagcag acctgaaagt ggttttgggg 1600
 aaattctacc gggatgatga ccgggatgag aagaccatcc agagcotaca 1650
 gatttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg 1700
 ctgacatcgc catcctgaag ctctagaca aggcccgat cagcaccgca 1750
 gtccagccca tctgctcgc tgccagtgg gatctcagca ctctctcca 1800
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 gccctggctt caagaacgac aactgcgct ctggggtgt cagtgtgtg 1900
 gactcgctgc tgtgtgagga gcagcatgag gaccatggca tccagtggag 1950
 tgtactgat aacatgttct gtgccagctg ggaaccact gcccttctg 2000
 atatctgcac tgacagaca ggagcatcg cggctgtgtc ctcccgga 2050
 cgagcatctc ctgagccagc ctggcatctg atgggactgg tcagctggag 2100
 ctatgataaa acatgacgcc acaggctctc cactgccttc accaagggtc 2150
 tgcttttaa agactggatt gaaagaaata tgaaatgaac catgctcatg 2200
 cactccttga gaagtgttc tgtatatccg tctgtactgt tgctattgcg 2250

Phe Val Met Leu Ser Leu Glu Phe Asp Tyr Met Cys Gln Tyr Asp	170	175	180
Tyr Val Glu Val Arg Asp Gly Asp Asn Arg Asp Gly Gln Ile Ile	185	190	195
Lys Arg Val Cys Gly Asn Glu Arg Pro Ala Pro Ile Gln Ser Ile	200	205	210
Gly Ser Ser Leu His Val Leu Phe His Ser Asp Gly Ser Lys Asn	215	220	225
Phe Asp Gly Phe His Ala Ile Tyr Glu Glu Ile Thr Ala Cys Ser	230	235	240
Ser Ser Pro Cys Phe His Asp Gly Thr Cys Val Leu Asp Lys Ala	245	250	255
Gly Ser Tyr Lys Cys Ala Cys Leu Ala Gly Tyr Thr Gly Gln Arg	260	265	270
Cys Glu Asn Leu Leu Glu Glu Arg Asn Cys Ser Asp Pro Gly Gly	275	280	285
Pro Val Asn Gly Tyr Gln Lys Ile Thr Gly Gly Pro Gly Leu Ile	290	295	300
Asn Gly Arg His Ala Lys Ile Gly Thr Val Val Ser Phe Phe Cys	305	310	315
Asn Asn Ser Tyr Val Leu Ser Gly Asn Glu Lys Arg Thr Cys Gln	320	325	330
Gln Asn Gly Glu Trp Ser Gly Lys Gln Pro Ile Cys Ile Lys Ala	335	340	345
Cys Arg Glu Pro Lys Ile Ser Asp Leu Val Arg Arg Arg Val Leu	350	355	360
Pro Met Gln Val Gln Ser Arg Glu Thr Pro Leu His Gln Leu Tyr	365	370	375
Ser Ala Ala Phe Ser Lys Gln Lys Leu Gln Ser Ala Pro Thr Lys	380	385	390
Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro Met Gly Tyr Gln His	395	400	405
Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser Pro Phe Tyr Arg	410	415	420
Arg Leu Gly Ser Ser Arg Arg Thr Cys Leu Arg Thr Gly Lys Trp	425	430	435
Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys Ile Glu	440	445	450
Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp Gln	455	460	465
Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu	470	475	480

<220>
<223> Synthetic oligonucleotide probe

<400> 233
tgtoaaggac gcactgccgt catg 24

<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
tggccagatc atcaagcgtg tctgtggcaa cgagcggccca gctcctatcc 50

<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
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agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt 100
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta 150
caaatccga ttactgttg tgttgacttt gtgcctgaca gtggttgggt 200
gggccaccag taactacttc gtgggtgccca ttcaagagat tcctaaagca 250
aaggagtcca tggctaattt ccataagacc ctcatcttgg ggaagggaaa 300
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc 350
cttctgtgtc tcttacctc agaggccaga gcaagctcat tttcaaacca 400
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg 450
ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg 500
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg 550
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca 600
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct 650
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat 700
gtggacctgg taoccgagaa tgactttaac ctttacaagt gtgaggagca 750
tcccaagcat ctgggtggtg gcaggaacag cactgggtac aggttacgtt 800
acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc 850
aagggtgaat gattctctaa caactactgg ggtatggggag gcgaagacga 900
tgacctcaga ctacagggtt agctccaaag aatgaaaatt tcccgcccc 950
tgcctgaagt gggtaaatat acaatggtct tocacactag agacaaaggc 1000

Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr
				20					25					30
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys
				35					40					45
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly
				50					55					60
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp
				65					70					75
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu
				80					85					90
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn
				95					100					105
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala
				110					115					120
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys
				125					130					135
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg
				140					145					150
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly
				155					160					165
Lys	Lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu
				170					175					180
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val
				185					190					195
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu
				200					205					210
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg
				215					220					225
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg
				230					235					240
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly
				245					250					255
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Glu
				260					265					270
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr
				275					280					285
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu
				290					295					300
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp
				305					310					315
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn
				320					325					330

098933 1203

214

tccctaccct ggcccagctc ctatctcaact aagaccgtcc tgaaagtctc 600
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 cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtccggt 2000
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 gttcttgccg cttttataag gccatcctag tccctgtctg ctggcagggg 2150

Tyr Asn Tyr Ser	Ile Ile Gly Thr Phe Thr Val Lys Leu Lys Val	200	205	210
Val Ala Glu Trp	Glu Glu Val Glu Pro Asp Ala Thr Arg Ala Val	215	220	225
Lys Gln Lys Thr	Gly Asp Phe Ser Ala Ser Leu Lys Leu Gln Glu	230	235	240
Thr Leu Arg Gly	Ile Gln Val Leu Gly Pro Thr Leu Ile Gln Thr	245	250	255
Phe Gln Lys Met	Thr Val Thr Leu Asn Phe Leu Gly Ser Pro Pro	260	265	270
Leu Thr Val Cys	Trp Arg Leu Lys Pro Glu Cys Leu Pro Leu Glu	275	280	285
Glu Gly Glu Cys	His Pro Val Ser Val Ala Ser Thr Ala Tyr Asn	290	295	300
Leu Thr His Thr	Phe Arg Asp Pro Gly Asp Tyr Cys Phe Ser Ile	305	310	315
Arg Ala Glu Asn	Ile Ile Ser Lys Thr His Gln Tyr His Lys Ile	320	325	330
Gln Val Trp Pro	Ser Arg Ile Gln Pro Ala Val Phe Ala Phe Pro	335	340	345
Cys Ala Thr Leu	Ile Thr Val Met Leu Ala Phe Ile Met Tyr Met	350	355	360
Thr Leu Arg Asn	Ala Thr Gln Gln Lys Asp Met Val Glu Asn Pro	365	370	375
Glu Pro Pro Ser	Gly Val Arg Cys Cys Cys Gln Met Cys Cys Gly	380	385	390
Pro Phe Leu Leu	Glu Thr Pro Ser Glu Tyr Leu Glu Ile Val Arg	395	400	405
Glu Asn His Gly	Leu Leu Pro Pro Leu Tyr Lys Ser Val Lys Thr	410	415	420
Tyr Thr Val				

<210> 242

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 242

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<210> 243

<211> 25

<212> DNA

<213> Artificial Sequence

[illegible]

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<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence
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<400> 244
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<210> 245
<211> 485
<212> DNA
<213> Homo sapiens
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<400> 245
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gctcccagat ctgggcccgt tgctctctgc tctctctctt cctcgccacg 100
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150
gcaaccccgag cagacagctg gagccaggcg cagctggatg cccatgtgtc 200
agaggcggaag gagggcgagac acccaacttc ccatctgcac ttctgtgtgc 250
ggctgtgtgc atogatcaaa gtgtgggtag tgctgcaaga cgtagaacct 300
acctgcctgc ccccgcgtcc ctcccttctt tatttatttc tgctgcccca 350
gaacatagtg cttggaaataa aatggctggg tcttttggtt tccaaaaaaa 400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485
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<210> 246
<211> 84
<212> PRT
<213> Homo sapiens
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400> 246														
Met	Ala	Leu	Ser	Ser	Gln	Ile	Trp	Ala	Ala	Cys	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Leu	Leu	Ala	Ser	Leu	Thr	Ser	Gly	Ser	Val	Phe	Pro	Gln	Gln
				20					25					30
Thr	Gly	Gln	Leu	Ala	Glu	Leu	Gln	Pro	Gln	Asp	Arg	Ala	Gly	Ala
				35					40					45
Arg	Ala	Ser	Trp	Met	Pro	Met	Phe	Gln	Arg	Arg	Arg	Arg	Arg	Asp
				50					55					60
Thr	His	Phe	Pro	Ile	Cys	Ile	Phe	Cys	Cys	Gly	Cys	Cys	His	Arg
				65					70					75

Ser Lys Cys Gly Met Cys Cys Lys Thr
80

<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

<400> 247
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tgctggcctg gcctggatct tccaccatgt toctgttgct gccttttgat 100
agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcacct 150
ccttctcgtt ttcacatag tgccagccat ttttgagtc tcctttggta 200
tcgcgaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250
ttgagaatgg agcaggaggc caaggagaag aaccaccago ttacaagcc 300
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caacactcca 400
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cctggaacct gctgagcaga accaattata acttccagta catcagcctt 550
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tgggcacaa tggtgtggga tacttgcaa atgggaggtt taaggaaatc 700
atgagtaaac atgttcactt aatgtgttac cggatctgcg tgcgagcgt 750
gacagccatc atcacotacc atgacaggga aaacagacca agaaatggtg 800
gcactctgtg ggccaatcat acctcacga tcgatgtgat catcttgcc 850
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tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950
gctcggaagt gaaggatgc cacctggttg ctaagagact gactgaacat 1000
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catcaataat acatcgtgta tgatgttcaa aaagggaagt tttgaaattg 1100
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ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300
gccattgcca ggcaggaggg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400
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 tgccctccagc tggctggggc caccgtgcgg ggtgccaaac ggctcagagc 1500
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 aactcccat gtgatgcgcg ctttgttgaa tgtgtgtctc gggttcccca 2150
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 ggtgaatga 2359

<210> 248
 <211> 456
 <212> PRT
 <213> Homo sapiens

<400> 248
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 Ile Val Pro Ala Ile Phe Gly Val Ser Phe Gly Ile Arg Lys Leu
 35 40 45
 Tyr Met Lys Ser Leu Leu Lys Ile Phe Ala Trp Ala Thr Leu Arg
 50 55 60
 Met Glu Arg Gly Ala Lys Glu Lys Asn His Gln Leu Tyr Lys Pro
 65 70 75

Tyr	Thr	Asn	Gly	Ile 80	Ile	Ala	Lys	Asp	Pro 85	Thr	Ser	Leu	Glu	Glu 90
Glu	Ile	Lys	Glu	Ile 95	Arg	Arg	Ser	Gly	Ser 100	Ser	Lys	Ala	Leu	Asp 105
Asn	Thr	Pro	Glu	Phe 110	Glu	Leu	Ser	Asp	Ile 115	Phe	Tyr	Phe	Cys	Arg 120
Lys	Gly	Met	Glu	Thr 125	Ile	Met	Asp	Asp	Glu 130	Val	Thr	Lys	Arg	Phe 135
Ser	Ala	Glu	Glu	Leu 140	Glu	Ser	Trp	Asn	Leu 145	Leu	Ser	Arg	Thr	Asn 150
Tyr	Asn	Phe	Gln	Tyr 155	Ile	Ser	Leu	Arg	Leu 160	Thr	Val	Leu	Trp	Gly 165
Leu	Gly	Val	Leu	Ile 170	Arg	Tyr	Cys	Phe	Leu 175	Leu	Pro	Leu	Arg	Ile 180
Ala	Leu	Ala	Phe	Thr 185	Gly	Ile	Ser	Leu	Leu 190	Val	Val	Gly	Thr	Thr 195
Val	Val	Gly	Tyr	Leu 200	Pro	Asn	Gly	Arg	Phe 205	Lys	Glu	Phe	Met	Ser 210
Lys	His	Val	His	Leu 215	Met	Cys	Tyr	Arg	Ile 220	Cys	Val	Arg	Ala	Leu 225
Thr	Ala	Ile	Ile	Thr 230	Tyr	His	Asp	Arg	Glu 235	Asn	Arg	Pro	Arg	Asn 240
Gly	Gly	Ile	Cys	Val 245	Ala	Asn	His	Thr	Ser 250	Pro	Ile	Asp	Val	Ile 255
Ile	Leu	Ala	Ser	Asp 260	Gly	Tyr	Tyr	Ala	Met 265	Val	Gly	Gln	Val	His 270
Gly	Gly	Leu	Met	Gly 275	Val	Ile	Gln	Arg	Ala 280	Met	Val	Lys	Ala	Cys 285
Pro	His	Val	Trp	Phe 290	Glu	Arg	Ser	Glu	Val 295	Lys	Asp	Arg	His	Leu 300
Val	Ala	Lys	Arg	Leu 305	Thr	Glu	His	Val	Gln 310	Asp	Lys	Ser	Lys	Leu 315
Pro	Ile	Leu	Ile	Phe 320	Pro	Glu	Gly	Thr	Cys 325	Ile	Asn	Asn	Thr	Ser 330
Val	Met	Met	Phe	Lys 335	Lys	Gly	Ser	Phe	Glu 340	Ile	Gly	Ala	Thr	Val 345
Tyr	Pro	Val	Ala	Ile 350	Lys	Tyr	Asp	Pro	Gln 355	Phe	Gly	Asp	Ala	Phe 360
Trp	Asn	Ser	Ser	Lys 365	Tyr	Gly	Met	Val	Thr 370	Tyr	Leu	Leu	Arg	Met 375
Met	Thr	Ser	Trp	Ala 380	Ile	Val	Cys	Ser	Val 385	Trp	Tyr	Leu	Pro	Thr 390

<220>
<223> Synthetic oligonucleotide probe

<400> 251
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<210> 252
<211> 1076
<212> DNA
<213> Homo sapiens

<400> 252
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gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac 150
tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200
tcaacacaac cctcttctg accatacagc cagaaggggg cactatcata 250
gtgacccaaa atcgtaatat ggagagagta gacttccacg atggaggcta 300
ctccctgaag ctacagcaaac tgaagaagaa tgactcaggg atctactatg 350
tggggatata cagctcatca ctccagcagc cctccaccca ggagtaactg 400
ctgcattgtc acgagcacct gtcaaacgct aaagtcacca tgggtctgca 450
gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac 500
atggggaaga ggatgtgatt tatacctgga agggcctggg gcaagcagcc 550
aatgagtcac ataattgggtc catcctcccc atctcctgga gatggggaga 600
aagtgatatg accttcattc gcgttgccag gaaccctgtc agcagaaact 650
tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac 700
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cagtctcttt gtaactgggc tatttctttg gttctgaag agagagagac 800
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cctaactatg gccccattc tggagagaac acagagtacg acacaatccc 900
tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950
ccactgtgga aatacogaaa aagatggaaa atccccactc actgctcagc 1000
atgccagaca caccaaggct atttcctat gagaatgta tctagacagc 1050
agtgcactcc cctaagtctc tgctca 1076

<210> 253
<211> 335
<212> PRT
<213> Homo sapiens

<400> 253
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		Val Lys Glu Leu	Val 30
Gly Ser Val Gly	Gly 35	Ala Val Thr Phe	Pro 40
		Leu Lys Ser Lys	Val 45
Lys Gln Val Asp	Ser 50	Ile Val Trp Thr	Phe 55
		Asn Thr Thr Pro	Leu 60
Val Thr Ile Gln	Pro 65	Glu Gly Gly Thr	Ile 70
		Ile Val Thr Gln	Asn 75
Arg Asn Arg Glu	Arg 80	Val Asp Phe Pro	Asp 85
		Gly Gly Tyr Ser	Leu 90
Lys Leu Ser Lys	Leu 95	Lys Lys Asn Asp	Ser 100
		Gly Ile Tyr Tyr	Val 105
Gly Ile Tyr Ser	Ser 110	Ser Leu Gln Gln	Pro 115
		Ser Thr Gln Glu	Tyr 120
Val Leu His Val	Tyr 125	Glu His Leu Ser	Lys 130
		Pro Lys Val Thr	Met 135
Gly Leu Gln Ser	Asn 140	Lys Asn Gly Thr	Cys 145
		Val Thr Asn Leu	Thr 150
Cys Cys Met Glu	His 155	Gly Glu Glu Asp	Val 160
		Ile Tyr Thr Trp	Lys 165
Ala Leu Gly Gln	Ala 170	Ala Asn Glu Ser	His 175
		Asn Gly Ser Ile	Leu 180
Pro Ile Ser Trp	Arg 185	Trp Gly Glu Ser	Asp 190
		Met Thr Phe Ile	Cys 195
Val Ala Arg Asn	Pro 200	Val Ser Arg Asn	Phe 205
		Ser Ser Pro Ile	Leu 210
Ala Arg Lys Leu	Cys 215	Glu Gly Ala Ala	Asp 220
		Asp Pro Asp Ser	Ser 225
Met Val Leu Leu	Cys 230	Leu Leu Leu Val	Pro 235
		Leu Leu Leu Ser	Leu 240
Phe Val Leu Gly	Leu 245	Phe Leu Trp Phe	Leu 250
		Lys Arg Glu Arg	Gln 255
Glu Glu Tyr Ile	Glu 260	Glu Lys Lys Arg	Val 265
		Asp Ile Cys Arg	Glu 270
Thr Pro Asn Ile	Cys 275	Pro His Ser Gly	Glu 280
		Asn Thr Glu Tyr	Asp 285
Thr Ile Pro His	Thr 290	Asn Arg Thr Ile	Leu 295
		Lys Glu Asp Pro	Ala 300
Asn Thr Val Tyr	Ser 305	Thr Val Glu Ile	Pro 310
		Lys Lys Met Glu	Asn 315
Pro His Ser Leu	Leu	Thr Met Pro Asp	Thr
		Pro Arg Leu Phe	Ala

330

<400> 255
gaaagacgtg gtcttgacag acagacaatc ctattcccta ccaaaatgaa 50

gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100
 aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150
 gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200
 acatggcaac tttagacttt ttctggagca aatccatgto ttggagaatt 250
 ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300
 tctatggttg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350
 tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400
 ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450
 gggctctatg gccgagaacc agatttgagt tcagacatca aggaaaggtt 500
 tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550
 tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600
 gcctccaatg ttgagtggac acttctcacc aggactccac catcatccct 650
 tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700
 ctgtctcact gagaagtcca attccagtct atcaacatgt tacctaggat 750
 acctcatcaa gaatcaaaga cttctttaa tttctctttg atacaccctt 800
 gacaattttt catgaaatta ttcctcttcc tgttcaataa atgattaccc 850
 ttgcacttaa 860

<210> 256
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 256
 Met Lys Met Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys
 1 5 10 15
 Val His Ala Glu Glu Ala Ser Ser Thr Gly Arg Asn Phe Asn Val
 20 25 30
 Glu Lys Ile Asn Gly Glu Trp His Thr Ile Ile Leu Ala Ser Asp
 35 40 45
 Lys Arg Glu Lys Ile Glu Glu His Gly Asn Phe Arg Leu Phe Leu
 50 55 60
 Glu Gln Ile His Val Leu Glu Asn Ser Leu Val Leu Lys Val His
 65 70 75
 Thr Val Arg Asp Glu Glu Cys Ser Glu Leu Ser Met Val Ala Asp
 80 85 90
 Lys Thr Glu Lys Ala Gly Glu Tyr Ser Val Thr Tyr Asp Gly Phe
 95 100 105
 Asn Thr Phe Thr Ile Pro Lys Thr Asp Tyr Asp Asn Phe Leu Met
 110 115 120

Ala His Leu Ile Asn Glu Lys Asp Gly Glu Thr Phe Gln Leu Met
 125 130
 Gly Leu Tyr Gly Arg Glu Pro Asp Leu Ser Ser Asp Ile Lys Glu
 140 145
 Arg Phe Ala Gln Leu Cys Glu Glu His Gly Ile Leu Arg Glu Asn
 155 160
 Ile Ile Asp Leu Ser Asn Ala Asn Arg Cys Leu Gln Ala Arg Glu
 170 175 180

<210> 257
 <211> 766
 <212> DNA
 <213> Homo sapiens

<400> 257
 ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg 50
 gacatcctgc aatggattca gctgtctggt tctactgctg ttaggagtag 100
 ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150
 tctcaaaacc ccatctcttg ctttgagtgg tgggtcccag gaattatagg 200
 agcagggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250
 aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300
 agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350
 ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450
 ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactggttt 500
 caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550
 gtttccactt cgattctgaa gaaaacaaac ataggcttat ccactttcca 600
 gtatttttag gtctattgct tgttgggaatt ctggagggtcc tgtttgggct 650
 cagtcagata gtcacgggtt tccttggtg tctgtgtgga gtctctaagc 700
 gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750
 gtttgaaaaa aaaaaa 766

<210> 258
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 258
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu
 1 5 10 15
 Leu Val Leu Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu
 20 25 30
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile

	35		40		45
Ser Cys Phe Glu	Trp 50	Trp Phe Pro Gly	Ile 55	Ile Gly Ala Gly	Leu 60
Met Ala Ile Pro	Ala 65	Thr Thr Met Ser	Leu 70	Thr Ala Arg Lys	Arg 75
Ala Cys Cys Asn	Asn 80	Arg Thr Gly Met	Phe 85	Leu Ser Ser Phe	Phe 90
Ser Val Ile Thr	Val 95	Ile Gly Ala Leu	Tyr 100	Cys Met Leu Ile	Ser 105
Ile Gln Ala Leu	Leu 110	Lys Gly Pro Leu	Met 115	Cys Asn Ser Pro	Ser 120
Asn Ser Asn Ala	Asn 125	Cys Glu Phe Ser	Leu 130	Lys Asn Ile Ser	Asp 135
Ile His Pro Glu	Ser 140	Phe Asn Leu Gln	Trp 145	Phe Phe Asn Asp	Ser 150
Cys Ala Pro Pro	Thr 155	Gly Phe Asn Lys	Pro 160	Thr Ser Asn Asp	Thr 165
Met Ala Ser Gly	Trp 170	Arg Ala Ser Ser	Phe 175	His Phe Asp Ser	Glu 180
Glu Asn Lys His	Arg 185	Leu Ile His Phe	Ser 190	Val Phe Leu Gly	Leu 195
Leu Leu Val Gly	Ile 200	Leu Glu Val Leu	Phe 205	Gly Leu Ser Gln	Ile 210
Val Ile Gly Phe	Leu 215	Gly Cys Leu Cys	Gly 220	Val Ser Lys Arg	Arg 225
Ser Gln Ile Val					

<210> 259
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 259
 gtogaatcca aatcactcat tgtgaaagct gagctcacag ccgaataagc 50
 caccatgagg ctgtcagtggt gtctctctgat ggtctcgctg gccctttgct 100
 gctaccaggc ccatgctctt gtctgccag ctgttgcttc tgagatcaca 150
 gtctctcttat tottaagtga cgctgcggta aacctccaag ttgccaaact 200
 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250
 ccgatcatgat atctttttaag aaacgactct cattgaaaaa gtcctgggtg 300
 aaatagttaa aaaatgtggt gtgtgacatg taaaaatgct caacctgggt 350
 tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaagggt 400

tcaacacggtt gctttaataa atcacttgcc ctgc 434

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

Met	Arg	Leu	Ser	Val	Cys	Leu	Leu	Met	Val	Ser	Leu	Ala	Leu	Cys
1				5				10					15	
Cys	Tyr	Gln	Ala	His	Ala	Leu	Val	Cys	Pro	Ala	Val	Ala	Ser	Glu
			20					25					30	
Ile	Thr	Val	Phe	Leu	Phe	Leu	Ser	Asp	Ala	Ala	Val	Asn	Leu	Gln
			35					40					45	
Val	Ala	Lys	Leu	Asn	Pro	Pro	Pro	Glu	Ala	Leu	Ala	Ala	Lys	Glu
			50					55					60	
Glu	Val	Lys	His	Cys	Thr	Asp	Gln	Ile	Ser	Phe	Lys	Lys	Arg	Leu
			65					70					75	
Ser	Leu	Lys	Lys	Ser	Trp	Trp	Lys							
			80											

<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

atccgttctc tgcgctgcc a gtcagggtga gccctcgcca aggtgacctc 50
gcaggacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg 100
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150
cgcccacgtg cctctccccc tgcagccctg cccctcgaac tgtgacatgg 200
agagagtgc cctggccctt ctctacttg caggcctgac tgccttgga 250
gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300
aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350
ggatcggcgg agttctgagt ggcaaatgca aatacaagag cagccagaag 400
cagcacagtc ctgtacctga gaaggccatc ccaactcatca ctccaggctc 450
tgccactact tgctgagcac aggactggcc tcagggatg gctgaagcc 500
taacactggc ccccagcacc tcctccctg ggaggcctta tcctcaagga 550
aggacttctc tccaagggca ggctgttagg ccctttctg atcaggaggc 600
ttctttatga attaaactcg cccaccacc ccctca 636

<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000
 agaggctgac accttcattg ttggaggcca tgacaccacg gccagtggcc 1050
 tctcctgggt cctgtacaac ctgcgaggc acccagaata ccaggagcgc 1100
 tgccgacagg aggtgcaaga gcttctgaag gaccgcgac ctaaagagat 1150
 tgaatgggac gacctggccc agctgccctt cctgacctg tgcgtgaagg 1200
 agagcctgag gttacatccc ccagctccct tcatctcccg atgtgcacc 1250
 caggacattg ttctcccaga tggccgagtc atcccaaaag gcattacctg 1300
 cctcatcgat attatagggg tccatcacaa cccaactgtg tggccggatc 1350
 ctgagggtcta cgaccccttc cgctttgacc cagagaacag caaggggagg 1400
 tcacctctgg cttttattcc tttctccgca gggcccagga actgcactcg 1450
 gcaggcggtc gccatggcgg agatgaaagt ggtcctggcg ttgatgctcg 1500
 tgcaattccg gttcctgccca gaccacactg agccccgcag gaagctggaa 1550
 ttgatcatgc gcgccgagg cgggccttgg ctgcgggtgg agccctgaa 1600
 ttaggcttg cagtgaactt ctgaccctc cacctgtttt ttgacagatt 1650
 gtcataata aaacggtgct gtcaaa 1676

<210> 264
 <211> 524
 <212> PRT
 <213> Homo sapiens

<400> 264
 Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala
 1 5 10 15
 Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu
 20 25 30
 Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys
 35 40 45
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe
 50 55 60
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys
 65 70 75
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val
 80 85 90
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp
 95 100 105
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys
 110 115 120
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly
 125 130 135

Ile Leu Leu Ser	Gly Gly Asp Lys Trp	Ser Arg His Arg Arg Met
140		145 150
Leu Thr Pro Ala	Phe His Phe Asn Ile	Leu Lys Ser Tyr Ile Thr
155		160 165
Ile Phe Asn Lys	Ser Ala Asn Ile Met	Leu Asp Lys Trp Gln His
170		175 180
Leu Ala Ser Glu	Gly Ser Ser Arg Leu	Asp Met Phe Glu His Ile
185		190 195
Ser Leu Met Thr	Leu Asp Ser Leu Gln	Lys Cys Ile Phe Ser Phe
200		205 210
Asp Ser His Cys	Gln Glu Arg Pro Ser	Glu Tyr Ile Ala Thr Ile
215		220 225
Leu Glu Leu Ser	Ala Leu Val Glu Lys	Arg Ser Gln His Ile Leu
230		235 240
Gln His Met Asp	Phe Leu Tyr Tyr Leu	Ser His Asp Gly Arg Arg
245		250 255
Phe His Arg Ala	Cys Arg Leu Val His	Asp Phe Thr Asp Ala Val
260		265 270
Ile Arg Glu Arg	Arg Arg Thr Leu Pro	Thr Gln Gly Ile Asp Asp
275		280 285
Phe Phe Lys Asp	Lys Ala Lys Ser Lys	Thr Leu Asp Phe Ile Asp
290		295 300
Val Leu Leu Leu	Ser Lys Asp Glu Asp	Gly Lys Ala Leu Ser Asp
305		310 315
Glu Asp Ile Arg	Ala Glu Ala Asp Thr	Phe Met Phe Gly Gly His
320		325 330
Asp Thr Thr Ala	Ser Gly Leu Ser Trp	Val Leu Tyr Asn Leu Ala
335		340 345
Arg His Pro Glu	Tyr Gln Glu Arg Cys	Arg Gln Glu Val Gln Glu
350		355 360
Leu Leu Lys Asp	Arg Asp Pro Lys Glu	Ile Glu Trp Asp Asp Leu
365		370 375
Ala Gln Leu Pro	Phe Leu Thr Met Cys	Val Lys Glu Ser Leu Arg
380		385 390
Leu His Pro Pro	Ala Pro Phe Ile Ser	Arg Cys Cys Thr Gln Asp
395		400 405
Ile Val Leu Pro	Asp Gly Arg Val Ile	Pro Lys Gly Ile Thr Cys
410		415 420
Leu Ile Asp Ile	Ile Gly Val His His	Asn Pro Thr Val Trp Pro
425		430 435
Asp Pro Glu Val	Tyr Asp Pro Phe Arg	Phe Asp Pro Glu Asn Ser
440		445 450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro
 455 460
 Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
 470 475 480
 Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His
 485 490 495
 Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly
 500 505 510
 Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln
 515 520

<210> 265
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 265
 caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50
 ctggcctcct gctgttttgc ttccacagga ttcttaaato ctctcttatt 100
 tttctctctc ctgactcca gggaaatatt ctttcaactc tcagcacctc 150
 atgaagacgc gcgcttaact ccggaggagc tagaaagagc ttcccttcta 200
 cagatattgc cagagatgct gggtgcagaa agaggggata ttctcaggaa 250
 agcagactca agtaccaca tttttaacct aagaggaaat ttgagaaagt 300
 ttcaggattt ctctggacaa gatcctaaca ttttactgag tcattctttg 350
 gccagaatct ggaaccata caagaaacgt gagactcctg attgcttctg 400
 gaaatactgt gtctgaagt aaataagcat ctgttagtca gctcagaaac 450
 acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagt 500
 tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550
 aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 266
 Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu
 1 5 10 15
 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
 20 25 30
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
 35 40 45
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
 50 55 60

Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
				65					70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
				80					85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
				95					100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
				110					115					

<210> 269
 <211> 1332
 <212> DNA
 <213> Homo sapiens

<400> 269
 cggccacagc tggcatgctc tgccatgatc ccatcctgct gtatgtcctc 50
 gtccagtacc tcgtgaaccc cgggggtgctc cgcacggacc ccagatgtca 100
 agaatatgaa cactgggctg ctgttcctcc ccctgttccc ggtgcagggtg 150
 cagaccctga tagtcgtgat catcgggatg ctctgtctcc tcttggaatt 200
 tcttggttg gtgcacctgg gccagctgct catcttcac atctacctga 250
 gtatgtcccc caccctaagc ccccgatccc cccaaggctg ggtggtcaga 300
 gctgctcacc ttacacctct acttgagtat gtccctaacc ctgagccccc 350
 cagcctctgg gccagagtct ttgtcccccg tgtgctgcatg tgttcagggt 400
 cagcctctcc cagaagtgg atcatggaca aaaagggcaa atcacaggaa 450
 gaaatataat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500
 gccgagacct gcaggagtgg tgccaggctg ttgaagtaac aagtttaaaa 550
 tgttcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600
 aaataaggac aggtggactt ccaaaaacac aagtagaagt tctaacaatg 650
 aaatatatta caggcaggct acccactaac caaacaactg aagcgagagc 700
 tgtgtcttg cttgtgtctc cagtgggcac agcggtaggc ggtcagtc 750
 gttgtgtaac gacggagggt aaactcccca gccccaagaa aaacctgtgt 800
 ggaagtaaca acaacctccc tgctcctggc accgacggtt ttggtcatgg 850
 tgggccagct gcaaagcgtc ttcattctc tgggcagttg tggccccgag 900
 gctgtggcct ctcagggggt ttctgtggac acgggcagca gagtgtgtcc 950
 aggccagccc ccaagaatgc cctgctcctg acagcttggc caaccctg 1000
 tcagggcaga gggagttggg tgggtcaggc tctgggctca cctccatctc 1050

cagagcatcc cctgcctgca gttgtggcaa gaacgcccag ctccagaatga 1100
 acacaccccca ccaagagcct cctgtgtcat aaccacaggt taccctacaa 1150
 accactgtcc ccacacaacc ctgggggatgt tttaaaacac acacctctaa 1200
 cgcatatctt acagtcaactg ttgtcttgcc tgagggttga atttttttta 1250
 atgaaagtgc aatgaaaatc actggattaa atccctacgga cacagagctg 1300
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332

<210> 270

<211> 142

<212> PRT

<213> Homo sapiens

<400> 270

Met	Asn	Thr	Trp	Leu	Leu	Phe	Leu	Pro	Leu	Phe	Pro	Val	Gln	Val
1				5					10				15	
Gln	Thr	Leu	Ile	Val	Val	Ile	Ile	Gly	Met	Leu	Val	Leu	Leu	Leu
				20					25				30	
Asp	Phe	Leu	Gly	Leu	Val	His	Leu	Gly	Gln	Leu	Leu	Ile	Phe	His
				35					40				45	
Ile	Tyr	Leu	Ser	Met	Ser	Pro	Thr	Leu	Ser	Pro	Arg	Ser	Pro	Gln
				50					55				60	
Gly	Trp	Val	Val	Arg	Ala	Ala	His	Leu	Thr	Pro	Leu	Leu	Glu	Tyr
				65					70				75	
Val	Pro	Asn	Pro	Glu	Pro	Pro	Thr	Pro	Gly	Ala	Arg	Val	Phe	Val
				80					85				90	
Pro	Arg	Val	Arg	Met	Cys	Ser	Gly	Ser	Ala	Ser	Pro	Arg	Ser	Glu
				95					100				105	
Ile	Met	Asp	Lys	Lys	Gly	Lys	Ser	Gln	Glu	Glu	Ile	Lys	Ser	Met
				110					115				120	
Arg	Thr	Gln	Gln	Ala	Gln	Gln	Glu	Ala	Glu	Leu	Thr	Pro	Arg	Pro
				125					130				135	
Ala	Gly	Val	Val	Pro	Gly	Ala								
				140										

<210> 271

<211> 1484

<212> DNA

<213> Homo sapiens

<400> 271

ggagtgcaga tggcatcctt cggttcttcc agacaagctg caagacgctg 50
 accatggcca agatggagct ctccgaaggcc ttctctggcc agcggagact 100
 cctatctgcc atcctcagca tgctatcact cagcttctcc acaacatccc 150
 tgctcagcaa ctactggttt gtgggcacac agaaggtgcc caagcccctg 200
 tgcgagaag gtctggcagc caagtgcctt gacatgccag tgtccctgga 250

tggagatacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300
 ctggggatga ccggtttctc ttccggagct tccggagtgg catgtggcta 350
 tcctgtgagg aaactgtgga agaaccaggg gagaggtgcc gaagtttcat 400
 tgaacttaca ccaccagcca agagaggtga gaaaggacta ctggaatttg 450
 ccacgttgca aggcccatgt caccccaactc tccgatttgg agggaagcgg 500
 ttgatggaga aggcttccct ccctccctc ccttggggc tttgtggcaa 550
 aaatcctatg gttatccctg ggaacgcaga tcacctacat cggacttcaa 600
 ttcacagct tctcctctgt actaacagac ttgtactca ctgggaaccc 650
 tgctgtggg ctcaaaactga gcgcctttgc tgtgtttcc tctgtcgtgt 700
 cagggtctct ggggatgggt gccacatga tgtattcaca agtcttcaa 750
 gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800
 tggctgggcc ttctacatgg cctggctctc cttcacctgc tgcattggcg 850
 cggctgtcac caccttcaac acgtacacca ggatgtgtct ggagttcaag 900
 tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taccacatca 950
 ccatcagtgt ttccctcggc ggctgtcaa tgcagcccc accgtgggtc 1000
 ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050
 gaggggagtgc acttctactc cgagctggcg aacaagggat ttcaaaggag 1100
 ggccagccag gagctgaaag aagcagttag gtcactgtga gaggaagagc 1150
 agtgtagga gtttaagcggg tttggggagt aggcttgagc cctaccttac 1200
 acgtctgctg attatcaaca tgtgcttaag ccaacatccg tctcttgagc 1250
 atggttttta gaggtacga ataaggctat gaataagggt tatctttaag 1300
 tcctaaggga ttctgggtg ccaactgctct ctttctctct acagctccat 1350
 cttgtttcac ccacccacac tctcacacat ccagaattcc ettccttact 1400
 gatagtttct gtgccaggtt ctgggctaaa ccatggagat aaaaagaaga 1450
 gtaaaatata cttcccagacc ttaagatct gaaa 1484

<210> 272

<211> 285

<212> PRT

<213> Homo sapiens

<400> 272

Met	Ala	Lys	Met	Glu	Leu	Ser	Lys	Ala	Phe	Ser	Gly	Gln	Arg	Thr
1					5					10				15
Leu	Leu	Ser	Ala	Ile	Leu	Ser	Met	Leu	Ser	Leu	Ser	Phe	Ser	Thr
				20					25					30
Thr	Ser	Leu	Leu	Ser	Asn	Tyr	Trp	Phe	Val	Gly	Thr	Gln	Lys	Val

accaaccagg gtagtggcat ggagcaccgt aaccatctgt gctctctgta 250
 tctctatgac agagccactt ctccacctct gaaatgttcc ctgctctgaa 300
 atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350
 cctgccttat tctctctccc aagtctgttc tcttattgtc aacctcagca 400
 caacaggctg gcgccaatgg cattacagag aaagcaatct gtgtggctag 450
 tgggcagatt accatgcaag cccaggaga aatggaggag cttttagacc 500
 acctccctgt cagccagtat taacatgtcc ccttccccct gccccgccgt 550
 agattcagga cattgcctcc tgtgtgccac caaaccagga ctttccccct 600
 ggcttggcat ccttggctct ctctgtgtac ccagcaagac gtctgttcca 650
 gggcagtgtg gcacttttca agctccgtta ctatggcgat ggcatgatg 700
 ttacaatccc acttgcctga ataataaagt gggaagggga agcagaggga 750
 aatggggcca tgtgaatgca gctgctctgt tctccctacc ctgaggaaaa 800
 accaaaggga agcaacagga acttctgcaa ctggttttta tcggaagagt 850
 catctgcct gcagatgctg ttgaaggggc acaagaaatg tagctggaga 900
 agattgatga aagtgcaggt gtgtaaggaa atagaacagt ctgctggagg 950
 tcagacctgg aattctgatt ccaaactctt tattactttg ggaagtcact 1000
 cagcctcccc gtagccatct ccagggtgac ggaaccaggt gtattacctg 1050
 ctggaaccaa ggaactaac aatgtaggtt actagtgaat accccaatgg 1100
 tttctccaat tatgcccatt ccaccaaac aataaacaa aattctctaa 1150
 cactgaaa 1158

<210> 274

<211> 86

<212> PRT

<213> Homo sapiens

<400> 274

Met	Trp	Leu	Pro	Leu	Gly	Leu	Leu	Ser	Leu	Cys	Leu	Ser	Pro	Leu
1					5				10					15
Pro	Ile	Leu	Ser	Ser	Pro	Ser	Leu	Lys	Ser	Gln	Ala	Cys	Gln	Gln
				20					25					30
Leu	Leu	Trp	Thr	Leu	Pro	Ser	Pro	Leu	Val	Ala	Phe	Arg	Ala	Asn
				35					40					45
Arg	Thr	Thr	Tyr	Val	Met	Asp	Val	Ser	Thr	Asn	Gln	Gly	Ser	Gly
				50					55					60
Met	Glu	His	Arg	Asn	His	Leu	Cys	Phe	Cys	Asp	Leu	Tyr	Asp	Arg
				65					70					75
Ala	Thr	Ser	Pro	Pro	Leu	Lys	Cys	Ser	Leu	Leu				
				80					85					

<210> 275
 <211> 2694
 <212> DNA
 <213> Homo sapiens

<400> 275
 gtagcgcgtc ttgggtctcc cggctgccgc tgctgccgc gccgcctcgg 50
 gtctgggagc caggagcgac gtcaccgcc tggcaggcat caaagctttg 100
 attagtttgt cctttggagg agcaatcgga ctgatgttt tgatgcttgg 150
 atgtgccctt ccaatataca acaaaactg gccctcttt gttctatttt 200
 tttacatctt ttcaacctatt ccatactgca tagcaagaag attagtggat 250
 gatacagatg ctatgagtaa cgcttgtaag gaacttgcca tctttcttac 300
 aacgggcatt gtctgttcag cttttggact cctattgta tttgccagag 350
 cacatctgat tgagtggga gcttgtgcac ttgttctcac aggaacacac 400
 gtcatctttg caactatact aggccttttc ttggtctttg gaagcaatga 450
 cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500
 atggacttcc tgtcatttgt tggccattca cgcacacagg agatggggc 550
 gtaaatgctg aatggtatag caagcctctt gggggatttt tagtgctcc 600
 cttctcactt ttattgtaag catactattt tcacagagac ttgctgaagg 650
 attaaaagga ttttctcttt tggaaaagct tgactgattt cacacttato 700
 tatagtatgc tttttgtggt gtctgtctga atttaaatat ttatgtgttt 750
 ttctgttag gttgattttt ttggaaatca atatgcaatg ttaaacaatt 800
 ttttaagtga atcatttgca ttggttagga attcagaatt ccgccggctc 850
 tattactggt caagtacatc ttttctctta aaattattta gcctccatta 900
 ttacaaaaaa ttataaaaat aagttttcag tcagtcagga tgacatcact 950
 cccaatgtta tgcagacata cagacgggtg gcatacgta tagactgtat 1000
 actcagtcca aatatagctg catttatacc tcagaggggc caagtgttaa 1050
 tgcccatgcc ctccgttaag ggtgttggt tttactggta gacagatgtt 1100
 ttgtggattg aaaattattt tatggaattg ctacagagga gtgcttttct 1150
 tctcaattgt tagaagaatt tatgttaaac ttttaaggtaa ggggttaaaa 1200
 acatttttga gataaggttt ttatttatgt ttattattgt tagagtgagt 1250
 tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300
 ctatttataa gtgaaatttg tgatctccta tcaacctttc atgttttacc 1350
 ctgttaaaat ggacatacat ggaaccacta ctgatgaggg acagttgtat 1400
 gtttgcatca tatatgccag aaaaccttcc tctgcttctt ccttttgact 1450

tatttgggtat gttgtatata ttacataaaa taacttttca aatatagttt 1500
 aataacactt agaagtgttt acttacctgg aaaaataattg ctatgccgta 1550
 cattcagagt gccccctccc ctgcaaggcc ttgccatgat taacaagtaa 1600
 ctgtttagtc ttacagataa ttcatgcatt aacagtttaa gatttagacc 1650
 atggtaaatag tagttcttat tctctaaggt tatatcatat gtaattttaa 1700
 agtattttta agacaagttt cotgtatacc tctgaactgt tttgattttg 1750
 agttcatcat gatagatctg ctgtttccct ataaaaggca tttgttgtgt 1800
 gagttaatgc aaagtagcca agtccagcta tatagcagct tcagaaacat 1850
 acotgaccaa aaaattccca gtaaccaggc atgatcaatt tatagtgttc 1900
 gtttcatctc aataattatc aggacttttt tcaggagtgg gttataaaaa 1950
 cattcaagtt ggtctgacag tattttgtta aggataattg tttgtatgtt 2000
 tattcagtat acttacataa aaattatttc gccatcagcc aaaactcagt 2050
 aatcatgaca gctgtctgtt gttttatgaa gtttatttct caagaaaatg 2100
 ggaataaatt tgggatttgt tcagcttttt tactaaagat gcctaaagcc 2150
 acaggtttta ttgcctaact taagccatga cttttagata tgagatgacg 2200
 ggaagcagga cgaaatatcg gcgtgtggct ggagcccttc cactggaggc 2250
 tgaaagtggc ttgtggtatt ataagtgtca gatttcaaga ggaaggtgca 2300
 ggtacacatg agttagagag ctggtgagac agttgggaac tctttgtgct 2350
 tgtgatctac tggacttttt ttttgaggga agtgcattct ctggctcttc 2400
 cctattttct gttctggatg tcagtgcagt gcactgotac tgttttatcc 2450
 acttggccac agactttttc taacagctgc gtattatttc tatatactaa 2500
 ttgcattggc agcatttgtt ctttgacctt gtatactagc ttgacatagt 2550
 gctgtctctg atttctaggc tagttacttg agatatgaat tttccataga 2600
 atatgcactg atacaacatt accattcttc tatggaaaga aaacttttga 2650
 tgatgaaaca ataaagattt taaatatcta ttttaaaaaa aaaa 2694

<210> 276

<211> 131

<212> PRT

<213> Homo sapiens

<400> 276

Met	Ala	Gly	Ile	Lys	Ala	Leu	Ile	Ser	Leu	Ser	Phe	Gly	Gly	Ala
1					5				10					15
Ile	Gly	Leu	Met	Phe	Leu	Met	Leu	Gly	Cys	Ala	Leu	Pro	Ile	Tyr
			20					25					30	
Asn	Lys	Tyr	Trp	Pro	Leu	Phe	Val	Leu	Phe	Phe	Tyr	Ile	Leu	Ser

	35		40		45
Pro Ile Pro Tyr	Cys Ile Ala Arg Arg	Leu Val Asp Asp Thr Asp			
	50	55	60		
Ala Met Ser Asn	Ala Cys Lys Glu Leu	Ala Ile Phe Leu Thr Thr			
	65	70	75		
Gly Ile Val Val	Ser Ala Phe Gly Leu	Pro Ile Val Phe Ala Arg			
	80	85	90		
Ala His Leu Ile	Glu Trp Gly Ala Cys	Ala Leu Val Leu Thr Gly			
	95	100	105		
Asn Thr Val Ile	Phe Ala Thr Ile Leu	Gly Phe Phe Leu Val Phe			
	110	115	120		
Gly Ser Asn Asp	Phe Ser Trp Gln Gln Trp				
	125	130			

<210> 277
 <211> 4104
 <212> DNA
 <213> Homo sapiens

<400> 277
 cccacgcgtc cgcccacgcg tcgcccacgc cgtccgccca cgcgtccgcc 50
 caccgcgtccg cccacgcgtc cgcccacgcg tcgggtgcaa gctcgccgcc 100
 cacactgcct ggtggaggga aggagcccg gcgcctctcg ccgctccccc 150
 cgccgcgctc cgcacctccc caccgcccgc cgcccgcgcg ccgcccgcgc 200
 caaagcatga gtgagcccg tcctctgcgc tgcccggggc gcgaatggca 250
 ggctgtttcc gcggagtaaa aggtggcgcc ggtcagtggt cgtttccaat 300
 gacggacatt aaccagactg tcagatcctg gggagtgcgc agccccgagt 350
 ttggagtttt ttccccccac aacgtcacag tcggaactgc agaggggaaa 400
 gaaggcgcca ggaaggcgaa gctcgggctc cggcacgtag ttgggaaact 450
 tgccgggtcct agaagtgcgc tccccgcctt gccggccgcg cttgcagccc 500
 cgagccgagc agcaaatga gacattgtgc gcctgccaga tcgcccgccc 550
 gcggaccggg gctgcctcgg aaacacagag gggctcttct tcgccctgca 600
 tataattagc ctgcacacaa agggagcagc tgaatggagg ttgtcactct 650
 ctggaaaagg atttctgacc gagcgcttcc aatggacatt ctccagtctc 700
 tctggaaaaga ttctcgctaa tggatttct gctgctcggt ctctgtctat 750
 actggctgct gaggaggccc tcgggggtgg tcttgtgtct gctggggggc 800
 tgctttcaga tgctccccgc cgccccacgc ggggtgccgc agctgtgcgc 850
 gtgcgagggg cggtgctgt actgcgagc gctcaacct accgagggcg 900
 cccacaaact gtccggcctg ctgggcttgt cctgcgcta caacagcctc 950

<210> 278
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 278

Met	Asp	Phe	Leu	Leu	Leu	Gly	Leu	Cys	Leu	Tyr	Trp	Leu	Leu	Arg	1	5	10	15
Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln	20	25	30	35
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys	40	45	50	55
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala	60	65	70	75
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	80	85	90	95
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln	100	105	110	115
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln	120	125	130	135
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu	140	145	150	155
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro	160	165	170	175
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln	180	185	190	195
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr	200	205	210	215
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile	220	225	230	235
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn	240	245	250	255
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys	260	265	270	275
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn	280	285	290	295
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu	300	305	310	315
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val	320	325	330	335
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr	340	345	350	355
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu	360	365	370	375

Gln	Leu	Asp	Ser	Asn	Arg	Leu	Thr	Tyr	Ile	Glu	Pro	Arg	Ile	Leu
				290					295					300
Asn	Ser	Trp	Lys	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Ala	Gly	Asn	Leu
				305					310					315
Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser
				320					325					330
Asn	Phe	Gln	Gly	Arg	Tyr	Asp	Gly	Asn	Leu	Gln	Cys	Ala	Ser	Pro
				335					340					345
Glu	Tyr	Ala	Gln	Gly	Glu	Asp	Val	Leu	Asp	Ala	Val	Tyr	Ala	Phe
				350					355					360
His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu
				365					370					375
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser
				380					385					390
Ala	Thr	Thr	Leu	Ala	Asp	Gly	Gly	Glu	Gly	Gln	His	Asp	Gly	Thr
				395					400					405
Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu
				410					415					420
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu
				425					430					435
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp
				440					445					450
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val
				455					460					465
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met
				470					475					480
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn
				485					490					495
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys
				500					505					510
Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val			
				515					520					

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

tcggtgcagg gggacgcctt tcagaaactg cgccgagtta aggaac 46

<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

Pro Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe
140 145 150

Arg Val Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser
155 160 165

Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala
170 175 180

Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro
185 190 195

Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly
200 205 210

Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala Ala
215 220 225

Leu Leu Gln Pro

<210> 282
<211> 644
<212> DNA
<213> Homo sapiens

<400> 282
atgcatcaaa ttgggagtag catcttcttc atgggaccag tgaacacgct 50
gaagcgaatg tttagccta ctcgtttgat tgcaactatc atggtgctgt 100
tgtgttttgc acttaccctg tgttctgcct ttgtgtggca taacaaggga 150
cttgcaactta tcttctgcat ttgacagtct ttggcattga cgtggtacag 200
cctttctctc ataccatttg caagggatgc tgtgaagaag tgttttgccg 250
tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta 300
tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct 350
tacagacatg tgccttttat ctgacagcaa tgtgttgctt gtgattcgaa 400
catttgaggg ttacttttgg aagcaacaat acattctoga acctgaatgt 450
cagtgcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt 500
cctcatgtac ctgtttcttc tctggatgtt gtcccactga attcccatga 550
atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 644

<210> 283
<211> 77
<212> PRT
<213> Homo sapiens

<400> 283
Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg
1 5 10 15
Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

aactcacgct catcctaatac ttactgttta caaaaaagaa gacgttccag 1150
aaaggtggca ttacaaatac aacagtcgaa ttcaaccaat catagcagtg 1200
gctgatgaag ggtggcacat ttacagaat aagtcagatg actttctgtt 1250
aggcaaccac ggttacgata atgcggttagc agatattgcat ccaatatttt 1300
tagcccatgg tctctgccttc agaaagaatt tctcaaaaga agccatgaac 1350
tccacagatt tgtaccocact actatgccac ctctcaata tcaactgcoat 1400
gccacacaat ggaatcattct ggaatgtcca ggatctgctc aattcagcaa 1450
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tattgaagtg gagattccat aattatgtca gtgtttaaag gtttcaaat 1750
ctgggaaacc agttccaaac atctgcagaa accattaagc agttacatat 1800
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atacttacac ctgcaaaagga ataaagatgt gagagtatgt ctccattgtt 1900
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tcttatttct ttccagagaa cgtggttttc atttattttt ccttcaaaaag 2350
agagtcacaa actgacagat togttctaaa tatattgttt ctgtcataaa 2400
attattgtga tttcctgatg agtcataatta ctgtgatttt cataataatg 2450
aagacaccat gaatatactt ttcttctata tagttcagca atggcctgaa 2500
tagaagcaac caggccacat ctacagcaatg ttttctcttg tttgtaatta 2550
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ggataaaaaa aaaaaaaaaa aaa 2623

<210> 285

098973 1203

252

290	295	300
Val Pro Glu Arg Trp His Tyr Lys Tyr	Asn Ser Arg Ile Gln Pro	
305	310	315
Ile Ile Ala Val Ala Asp Glu Gly Trp	His Ile Leu Gln Asn Lys	
320	325	330
Ser Asp Asp Phe Leu Leu Gly Asn His	Gly Tyr Asp Asn Ala Leu	
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala	His Gly Pro Ala Phe Arg	
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn	Ser Thr Asp Leu Tyr Pro	
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr	Ala Met Pro His Asn Gly	
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu	Asn Ser Ala Met Pro Arg	
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile	Leu Leu Pro Gly Ser Val	
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly	Ser Tyr Pro Tyr Phe Ile	
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val	Ile Val Phe Phe Val Ile	
440	445	450
Phe Ile Lys His Leu Ile His Ser Gln	Ile Pro Ala Leu Gln Asp	
455	460	465
Met His Ala Glu Ile Ala Gln Pro Leu	Leu Gln Ala	
470	475	

<210> 286
 <211> 1337
 <212> DNA
 <213> Homo sapiens

<400> 286
 ggatttttgt gatccggat tcgctccac gggcgggacc tttgtaactg 50
 cgggaggccc aggacagccc caccctgcgg ggccggaggc agccgggggtg 100
 agggaggtga agaaaccaag acgcagagag gccaaagcccc ttgccttggtg 150
 tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200
 aacaggggaca tggccacctg ggacgaaaag gcagtcaccc gcaggggccaa 250
 ggtggctccc gctgagagga tgagcaagtt ctttaaggcac ttcacgggtcg 300
 tgggagacga ctaccatgcc tggaacatca actacaagaa atggggagaat 350
 gaagaggagg aggaggagga ggagcagcca cccccacac cagtctcagg 400
 cgagggaagg agagctgcag cccctgacgt tgccccctgcc cctggccccg 450
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tcccacaggt ttcaggtcat catcatctgc ttggtgggtc tggatgcctt 550
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 agaataaacta tgctgccatg gtattccact acatgagcat caccatcttg 650
 gtctttttta tgatggagat catctttaa tttttgtct tccgcctgag 700
 ttctttcacc acaagtttga gatcctggat gcccgctgtg gtggtgtgct 750
 cattcatcct ggacattgtc ctctgttcc aggagcacca gtttgaggct 800
 ctgggcctgc tgattctgct ccggtgtgtg cgggtggccc ggatcatcaa 850
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 aggagaagct ctctccggat ggctatggga atgaaagaat ccgacttcta 1050
 ctctcacaca gccaccgtga aagtcctgga gtaaaatgtg ctgtgtacag 1100
 aagagagaga aggaagcagg ctggcatgtt cactgggctg gtgttacgac 1150
 agagaacctg acagtcactg gccagttatc acttcagatt acaaatcaca 1200
 cagagcatct gcctgttttc aatcacaga gaacaaaacc aaaatctata 1250
 aagatattct gaaaatatga cagaatttga caaataaaag cataaacgtg 1300
 taaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaa 1337

<210> 287
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 287
 Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val
 1 5 10
 Ala Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val
 20 25 30
 Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp
 35 40 45
 Glu Asn Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr
 50 55 60
 Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Pro Asp Val Ala
 65 70 75
 Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly
 80 85 90
 Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile
 95 100 105
 Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu
 110 115 120

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala
				125					130					135
Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe
				140					145					150
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser
				155					160					165
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val
				170					175					180
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe
				185					190					195
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala
				200					205					210
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu
				215					220					225
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala
				230					235					240
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp
				245					250					255

<210> 288
 <211> 3334
 <212> DNA
 <213> Homo sapiens

<400> 288
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 cccagaccga gttccagtac tttagtcga aggggctccc tgcgagctg 150
 aagtccattt tcaagctcag tgtcttcac cctcccagg aattctccac 200
 ctaccgccag tggaagcaga aaattgtaca agctggagat aaggacctg 250
 atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag 300
 aagaagctga ggctggtgtt taagatttg gacaaaaaga atgatggacg 350
 cattgacgag caggagatca tgcagtcctt gcgggacttg ggagtcaaga 400
 tatctgaaca gcaggcagaa aaaattctca agagcatgga taaaaacggc 450
 acgatgacca tcgactggaa cgagtgagga gactaccacc tcctccacc 500
 cgtgaaaac atccccgaga tcactctcta ctggaagcat tccacgatct 550
 ttgatgtggg tgagaatcta acggtcccg atgagttcac agtggaggag 600
 aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650
 ggccgtatcc agaacctgca cggccccctt ggacaggtct aaggtgctca 700
 tgcaggtcca tgctcccg agcaacaaca tgggcatcgt tggtggcttc 750

aaagggtttt gtccagaagg acaagccgga caaatgagcg acttctgtgc 2400
 ttccagagga agacgaggga gcaggagctt ggctgactgc tcagagtctg 2450
 ttctgacgcc ctgggggttc ctgtccaacc ccagcagggg cgagcgggga 2500
 ccagcccac attccacttg tgtcactgct tggaacctat ttattttgta 2550
 tttatttgaa cagagttatg tcttaactat ttttatagat ttgtttaatt 2600
 aatagcttgt cattttcaag ttcatttttt attcatattt atgttcatgg 2650
 ttgattgtac cttcccaagc ccgcccagtg ggatgggagg aggaggagaa 2700
 ggggggcctt gggccgctgc agtcacatct gtccagagaa attccttttg 2750
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 aatccagtta tttcctgcgc tgcgagggtt tctttatttc actcctttct 2950
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 ggctggagga gagggtgggg ggctggctcc gtccctccca gccttctgct 3050
 gcccttgctt aacaatgccg gccaaactgc gacctcacgg ttgcacttcc 3100
 attccaccag aatgacctga tgaggaaatc ttcaatagga tgcaaatgac 3150
 aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca 3200
 aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta 3250
 ataaagtgtg ttcaagctg aaaaaaaaa aaaaaaaaa aaaaaaaaa 3300
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa 3334

<210> 289

<211> 469

<212> PRT

<213> Homo sapiens

<400> 289

Met	Leu	Cys	Leu	Cys	Leu	Tyr	Val	Pro	Val	Ile	Gly	Glu	Ala	Gln
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Thr	Glu	Phe	Gln	Tyr	Phe	Glu	Ser	Lys	Gly	Leu	Pro	Ala	Glu	Leu
			20						25					30
Lys	Ser	Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe
			35						40					45
Ser	Thr	Tyr	Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp
			50						55					60
Lys	Asp	Leu	Asp	Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr
			65						70					75
Leu	Gln	Asp	His	Glu	Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ile	Leu
			80						85					90

Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu Val Thr Met Ser
 410 415 420

Ser Leu Phe Lys His Ile Leu Arg Thr Glu Gly Ala Phe Gly Leu
 425 430 435

Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro Ala Val
 440 445 450

Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu Gly
 455 460 465

Val Gln Ser Arg

<210> 290
 <211> 1658
 <212> DNA
 <213> Homo sapiens

<400> 290
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 gcatcatcat tattctggct ggagcaattg cactcatcat tggctttggt 150
 atttcaggga gacactccat cacagtcaact actgtcgct cagctgggaa 200
 cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250
 ttctgatata cgtgatacaa tggctgaagg aagtggtttt aggcttggtc 300
 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 350
 cagaggccgg acagcagtg ttgctgatca agtgatagtt ggcaatgcct 400
 ctttgccgct gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450
 tatatcatca cttctaaagg caaggggaat gtaaccttg agtataaac 500
 tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550
 agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtggtc 600
 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650
 cagcttttag ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc 700
 tctacaatgt tacgatcaac aacacatact cctgtatgat tgaatatgac 750
 attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaaag 800
 gcggagtca ctcagctgc taaactcaaa ggcttctctg tgtgtctctt 850
 ctttctttgc catcagctgg gcaacttctg ctctcagccc ttacctgatg 900
 ctaaaataat gtgccttggc cacaaaaaag catgcaaagt cattgttaca 950
 acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000
 ttctgggagg aaatgaattc atatctagaa gtctggagtg agcaacaacg 1050

agcaagaaac aaaagaagc caaaagcaga aggctccaat atgaacaaga 1100
 taatctatc ttaaagaca tattagaagt tgggaaaata attcatgtga 1150
 actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200
 gcatcccccag atctcaggga cctcccctg cctgtcacct ggggagtgtg 1250
 aggacaggat agtgcattgt ctttgtctct gaatttttag ttatatgtgc 1300
 tgtaatgttg ctctgaggaa gcccttgaa agtctatccc aacatatcca 1350
 catcttatat tccacaaatt aagctgtagt atgtacccta agacgctgct 1400
 aattgactgc cacttcgcaa ctcaggggag gctgcatttt agtaatgggt 1450
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500
 ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550
 acagagcagt cggggacacc gattttataa ataaactgag caccttcttt 1600
 ttaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaa 1658

<210> 291
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 291
 Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile 15
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 Ile Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly 30
 20 25
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala 45
 35 40
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro 60
 50 55
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly 75
 65 70
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu 90
 80 85
 Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala 105
 95 100
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val 120
 110 115
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser 135
 125 130
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe 150
 140 145
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr

gcccctgggc catgaagtgc tggcagtgag cggatggacc tagcacttcc 850
 cctctctggc cttagcttcc tcctctctta tggggataac agctacctca 900
 tggatcacaa taagagaaca agagtgaag agttttgtaa ccttcaagt 950
 ctgttcagct gcggggattt agcacaggag actctacgct caccctcagc 1000
 aacctttctg cccacgagc tctcttctg ctaacatctc aggtctccag 1050
 cccagccacc attactgtg cctgatctg actatcatg tggcaggttc 1100
 catggactgc agaactccag ctgcatggaa agggccagct gcagactttg 1150
 agccagaaat gcaaacggga ggcctctggg actcagtcag agcgctttg 1200
 ctgaatgagg ggtggaaccg agggaagaag gtgcgtcgga gtggcagatg 1250
 caggaaatga gctgtctatt agccttgct gccccacca ttaggtaggc 1300
 agaaatctc actgccagcc cctcttaaac aggtagagag ctgtgagccc 1350
 cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400
 ctatgtaaac agacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 293
 Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala
 1 5 10 15
 Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala
 20 25 30
 Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu
 35 40 45
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro
 50 55 60
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu
 65 70 75
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu
 80 85 90
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp
 95 100 105
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln
 110 115 120
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro
 125 130 135
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro
 140 145 150

Phe Pro Leu Gln Leu Phe Cys Phe Leu Val Ala Ile Arg Val Pro
155 160 165

Phe Pro Trp Thr Val Trp Arg Lys Thr Glu Ala Gly Val Trp Asp
170 175 180

<210> 294
<211> 1164
<212> DNA
<213> Homo sapiens

<400> 294
cttctgtagg acagtcacca ggccagatcc agaagcctct ctaggctcca 50
gctttctctg tggaagatga cagcaattat agcaggaccc tgcaggctg 100
tcgaaaagat tccgcaataa aactttgcca gtgggaagta cctagtga 150
cggcctaaga tggcacttct tctcatgtcc caggcttgag gccctgtggt 200
ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctcgtt 250
gctggtatca ctgcagtgtc tgttgtagct gtagaatctc ttagctgcgt 300
gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcccttgaat 350
gtccctcaca tggcaacacc agctgtatca gctcctcagc cagctcctct 400
ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450
ctgcagtgtg gagacacaca ttacagcctt cactgtccac gtgtctgtgt 500
aagaacactt tcattttgta agccagtgtc gccaaaggaaa ggaatgcagc 550
aacaccagcg atgccctgga cctccctctg aagaacgtgt ccagcaacgc 600
agagtgcctt gcttggtatg aatctaattg aacttctgt cgtgggaagc 650
cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700
aagaatgaca ttgagtctaa gagtctctgt ctgaaaggct gttccaacgt 750
cagtaacgcc acctgtcagt tctgtctgtg tgaaaacaag actcttgagg 800
gagtcatctt togaagttt gagtgtgcaa atgtaaacag ctttaacccc 850
acgtctgcac caaccacttc ccacaacgtg ggctccaaag ctccctctca 900
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ttgttcttca ttattaaagc actggttcat tcaactgcca aaaaaaaaaa 1150
aaaaaaaaaa aaaa 1164

<210> 295
<211> 237
<212> PRT

<213> Homo sapiens

<400> 295

Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala
1 5 10 15

Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys
20 25 30

Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
35 40 45

Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
50 55 60

Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
65 70 75

Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
80 85 90

Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
95 100 105

Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
110 115 120

Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
125 130 135

Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
140 145 150

Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
155 160 165

Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
170 175 180

Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
185 190 195

Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
200 205 210

Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
215 220 225

Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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ccagcccat ggtcccgcc gccggcgcg tgctgtgggt cctgctgctg 150

aatctgggtc cccggcggc gggggcccaa ggctgaccc agactccgac 200
 cgaaatgcag cgggtcagtt tacgctttgg gggcccatg acccgcgact 250
 accggagcac cgcccgact ggtcttcccc ggaagacaag gataatccta 300
 gaggacgaga atgatgccat ggccgacgcc gaccgcctgg ctggaccagc 350
 ggctgccgag ctcttgccg ccacgggtgc caccgcttt agccggctgt 400
 ccgccattaa cgaggaggat gggctctcag aagaggggtg tgtgattaat 450
 gccggaaagg atagcaccag cagagagctt cccagtgcga ctccaatac 500
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 gcgccttcga gttggggcgc tgagccagct ccgcacggag cacaagcctt 850
 gcacctatca acaatgtccc tgcaaccgac ttcgggaaga gtgccccctg 900
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 agagatgcaa ccaatagaca gaaaccagag gtaatggcca ctccatccac 1150
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 ccactagata tttttagtac agaaaaacaa aactggaaaa caca 1245

<210> 297
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Asn
 1 5 10 15
 Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro
 20 25 30
 Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr
 35 40 45
 Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr
 50 55 60
 Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp

	65		70		75
Arg Leu Ala Gly	Pro Ala Ala Ala Glu	Leu Leu Ala Ala Thr	Val		
	80	85	90		
Ser Thr Gly Phe	Ser Arg Ser Ser Ala	Ile Asn Glu Glu Asp	Gly		
	95	100	105		
Ser Ser Glu Glu Gly	Val Val Ile Asn Ala	Gly Lys Asp Ser Thr			
	110	115	120		
Ser Arg Glu Leu	Pro Ser Ala Thr Pro	Asn Thr Ala Gly Ser	Ser		
	125	130	135		
Ser Thr Arg Phe	Ile Ala Asn Ser Gln	Glu Pro Glu Ile Arg	Leu		
	140	145	150		
Thr Ser Ser Leu	Pro Arg Ser Pro Gly	Arg Ser Thr Glu Asp	Leu		
	155	160	165		
Pro Gly Ser Gln	Ala Thr Leu Ser Gln	Trp Ser Thr Pro Gly	Ser		
	170	175	180		
Thr Pro Ser Arg	Trp Pro Ser Pro Ser	Pro Thr Ala Met Pro	Ser		
	185	190	195		
Pro Glu Asp Leu	Arg Leu Val Leu Met	Pro Trp Gly Pro Trp	His		
	200	205	210		
Cys His Cys Lys	Ser Gly Thr Met Ser	Arg Ser Arg Ser Gly	Lys		
	215	220	225		
Leu His Gly Leu	Ser Gly Arg Leu Arg	Val Gly Ala Leu Ser	Gln		
	230	235	240		
Leu Arg Thr Glu	His Lys Pro Cys Thr	Tyr Gln Gln Cys Pro	Cys		
	245	250	255		
Asn Arg Leu Arg	Glu Glu Cys Pro Leu	Asp Thr Ser Leu Cys	Thr		
	260	265	270		
Asp Thr Asn Cys	Ala Ser Gln Ser Thr	Thr Ser Thr Arg Thr	Thr		
	275	280	285		
Thr Thr Pro Phe	Pro Thr Ile His Leu	Arg Ser Ser Pro Ser	Leu		
	290	295	300		
Pro Pro Ala Ser	Pro Cys Pro Ala Leu	Ala Phe Trp Lys Arg	Val		
	305	310	315		
Arg Ile Gly Leu	Glu Asp Ile Trp Asn	Ser Leu Ser Ser Val	Phe		
	320	325	330		
Thr Glu Met Gln	Pro Ile Asp Arg Asn	Gln Arg			
	335	340			

<210> 298
 <211> 2692
 <212> DNA
 <213> Homo sapiens

<400> 298
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 cgaccgtgag ccggtgtacc gcgactcggt actgcagtgc gaagagcaga 150
 actgctcttg gggcgctctg aatcaacttc gctcccgcga gccaatctac 200
 atgagtctag caggetggac ctgtcgggac gactgtaagt atgagtgtat 250
 gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300
 tccatggcaa gtggcccttc tcccggttcc tgttctttca agagccggca 350
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 cacaccaggg acactgacct cacagagaaa atggactact tctgtgcctc 550
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 caacctgtgt gccaacgtgg ctattggcct ggtcaacgtg gtgtgtggcg 750
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 ctgtacctgc tgaaggaaac agaggacaag ttcaagctgg actgaagacc 1000
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 ttggccctca ccagccttgg agtctgttct aggggaaggc tcccagcctc 1200
 tgggactcga gagtgggcag cccctctacc tcttgagct gaactggggt 1250
 ggaactgagt gtgttcttag ctctacgggg aggcacagct cctgtttcct 1300
 cccaccagc ctctctccca catccccagc tgcctggctg ggtcctgaag 1350
 ccctctgtct acctgggaga ccagggaacca caggccttag ggatacaggg 1400
 ggtccccctc tgttaaccac ccccaacctc ctccaggaac cactaggtg 1450
 gtgctggatg cttgttcttt ggccagcga ggttcacggc gattctcccc 1500
 atgggatctt gagggaccaa gctgctggga ttgggaagga gtttcaacct 1550
 gaccgttgcc ctagccaggt tcccaggag cctcaccata ctccctttca 1600
 gggccagggc tccagcaagc ccagggaag gatcctgtgc tgtgtctgtg 1650

Thr	Val	Gly	Leu	Tyr	Leu	Gln	Glu	Gly	His	Lys	Val	Pro	Gln	Phe	
				80					85					90	
His	Gly	Lys	Trp	Pro	Phe	Ser	Arg	Phe	Leu	Phe	Phe	Gln	Glu	Pro	
				95					100					105	
Ala	Ser	Ala	Val	Ala	Ser	Phe	Leu	Asn	Gly	Leu	Ala	Ser	Leu	Val	
				110					115					120	
Met	Leu	Cys	Arg	Tyr	Arg	Thr	Phe	Val	Pro	Ala	Ser	Ser	Pro	Met	
				125					130					135	
Tyr	His	Thr	Cys	Val	Ala	Phe	Ala	Trp	Val	Ser	Leu	Asn	Ala	Trp	
				140					145					150	
Phe	Trp	Ser	Thr	Val	Phe	His	Thr	Arg	Asp	Thr	Asp	Leu	Thr	Glu	
				155					160					165	
Lys	Met	Asp	Tyr	Phe	Cys	Ala	Ser	Thr	Val	Ile	Leu	His	Ser	Ile	
				170					175					180	
Tyr	Leu	Cys	Cys	Val	Arg	Thr	Val	Gly	Leu	Gln	His	Pro	Ala	Val	
				185					190					195	
Val	Ser	Ala	Phe	Arg	Ala	Leu	Leu	Leu	Leu	Met	Leu	Thr	Val	His	
				200					205					210	
Val	Ser	Tyr	Leu	Ser	Leu	Ile	Arg	Phe	Asp	Tyr	Gly	Tyr	Asn	Leu	
				215					220					225	
Val	Ala	Asn	Val	Ala	Ile	Gly	Leu	Val	Asn	Val	Val	Trp	Trp	Leu	
				230					235					240	
Ala	Trp	Cys	Leu	Trp	Asn	Gln	Arg	Arg	Leu	Pro	His	Val	Arg	Lys	
				245					250					255	
Cys	Val	Val	Val	Val	Leu	Leu	Leu	Gln	Gly	Leu	Ser	Leu	Leu	Glu	
				260					265					270	
Leu	Leu	Asp	Phe	Pro	Pro	Leu	Phe	Trp	Val	Leu	Asp	Ala	His	Ala	
				275					280					285	
Ile	Trp	His	Ile	Ser	Thr	Ile	Pro	Val	His	Val	Leu	Phe	Phe	Ser	
				290					295					300	
Phe	Leu	Glu	Asp	Asp	Ser	Leu	Tyr	Leu	Leu	Lys	Glu	Ser	Glu	Asp	
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				320											

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 <212> DNA
 <213> Homo sapiens

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<210> 301

<211> 461
 <212> PRT
 <213> Homo sapiens

<400> 301

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Ser	His	Gln	Asn	Leu	Lys	Glu	Phe	Ala	Leu	Thr	Asn	Pro	Glu	Lys	35	40	45	
Ser	Ser	Thr	Lys	Glu	Thr	Glu	Arg	Lys	Glu	Thr	Lys	Ala	Glu	Glu	50	55	60	
Glu	Leu	Asp	Ala	Glu	Val	Leu	Glu	Val	Phe	His	Pro	Thr	His	Glu	65	70	75	
Trp	Gln	Ala	Leu	Gln	Pro	Gly	Gln	Ala	Val	Pro	Ala	Gly	Ser	His	80	85	90	
Val	Arg	Leu	Asn	Leu	Gln	Thr	Gly	Glu	Arg	Glu	Ala	Lys	Leu	Gln	95	100	105	
Tyr	Glu	Asp	Lys	Phe	Arg	Asn	Asn	Leu	Lys	Gly	Lys	Arg	Leu	Asp	110	115	120	
Ile	Asn	Thr	Asn	Thr	Tyr	Thr	Ser	Gln	Asp	Leu	Lys	Ser	Ala	Leu	125	130	135	
Ala	Lys	Phe	Lys	Glu	Gly	Ala	Glu	Met	Glu	Ser	Ser	Lys	Glu	Asp	140	145	150	
Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	Pro	Ile	Glu	155	160	165	
Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	Glu	Thr	170	175	180	
Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	Ser	185	190	195	
Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	200	205	210	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	215	220	225	
Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	230	235	240	
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	245	250	255	
Ser	Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	260	265	270	
Gln	Lys	Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	275	280	285	
Lys	Lys	Lys	Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe				

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<210> 303
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 303
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 20 25 30
 Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser
 35 40 45
 Leu Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr
 50 55 60
 Asp Arg Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly
 65 70 75
 Ala Ala Val Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr
 80 85 90
 Tyr Lys Leu Leu Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser
 95 100 105
 Glu Asp Gly Arg Ser Pro Ile Ser Ile Arg Gln Met Ala Tyr Val
 110 115 120
 Ser Gly Leu Ser Phe Gly Ile Ile Ser Gly Val Phe Ser Val Ile
 125 130 135
 Asn Ile Leu Ala Asp Ala Leu Gly Pro Gly Val Val Gly Ile His
 140 145 150
 Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser Ala Phe Leu Thr Ala
 155 160 165
 Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val Val Phe Phe Asp
 170 175 180
 Ala Cys Glu Arg Arg Tyr Trp Ala Leu Gly Leu Val Val Gly
 185 190 195
 Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro Trp Tyr
 200 205 210
 Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met Gly
 215 220 225
 Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
 230 235 240
 Arg Ser Leu Leu Cys Lys Asp
 245

<210> 304
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
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aagatcaacc catttccatt ccgcagatg gcctatgttt ctggtctctc 100
ccttcggnat catcagtggt gtntntctg ttatcaatat ttggcgtgat 150
gcanttgggc caggtgtggt tgggacatc ggagactcac cctattantt 200
cctganttca gccttntga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
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ctgcttaaga aggcagatga ggggttagca tngctgagt aggacggaga 150
atcacocatt tccatccgcc agatggccta tgtttntggt ntttcctcg 200
gtatcatcag tgggtgtttt tctgttatca atattttggn tgatgcantt 250
gggccagtg tggttgggat ccatggagan taccctatt aattcctgaa 300
ttcagccttt ntgcacgcag ccattatcct gntccatacc ttttggggag 350
ttgtgttttt tgatgcctgt gagaggag 378

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
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ctgcggtgtt ttctggctgc actttctctg cgttcggccc ggccttcctg 250

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 ctggtgaggg tggctcagca ggcagggaag gagaggtgtc tgtgcgtcct 200
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 ggtggcccg ccttgtggtt cctctctacc tggggaata aggtgcagcg 350
 gccatggcta cagcaagacc ccctggatg tgggtgctct gtgctctgat 400
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 ctgggagctg gggcgggga agacgcccgg tcggatgaca gcagcagcgg 550
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<210> 309

<211> 293
 <212> PRT
 <213> Homo sapiens

<400> 309

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Ile	Thr	Ala	Leu	Leu	Leu	Gly	Val	Thr	Glu	His	Val	Leu	Ala	Asn
			20						25					30
Asn	Asp	Val	Ser	Cys	Asp	His	Pro	Ser	Asn	Thr	Val	Pro	Ser	Gly
			35						40					45
Ser	Asn	Gln	Asp	Leu	Gly	Ala	Gly	Ala	Gly	Glu	Asp	Ala	Arg	Ser
			50						55					60
Asp	Asp	Ser	Ser	Ser	Arg	Ile	Ile	Asn	Gly	Ser	Asp	Cys	Asp	Met
			65						70					75
His	Thr	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Leu	Leu	Arg	Pro	Asn	Gln
			80						85					90
Leu	Tyr	Cys	Gly	Ala	Val	Leu	Val	His	Pro	Gln	Trp	Leu	Leu	Thr
			95						100					105
Ala	Ala	His	Cys	Arg	Lys	Lys	Val	Phe	Arg	Val	Arg	Leu	Gly	His
			110						115					120
Tyr	Ser	Leu	Ser	Pro	Val	Tyr	Glu	Ser	Gly	Gln	Gln	Met	Phe	Gln
			125						130					135
Gly	Val	Lys	Ser	Ile	Pro	His	Pro	Gly	Tyr	Ser	His	Pro	Gly	His
			140						145					150
Ser	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asn	Arg	Arg	Ile	Arg	Pro
			155						160					165
Thr	Lys	Asp	Val	Arg	Pro	Ile	Asn	Val	Ser	Ser	His	Cys	Pro	Ser
			170						175					180
Ala	Gly	Thr	Lys	Cys	Leu	Val	Ser	Gly	Trp	Gly	Thr	Thr	Lys	Ser
			185						190					195
Pro	Gln	Val	His	Phe	Pro	Lys	Val	Leu	Gln	Cys	Leu	Asn	Ile	Ser
			200						205					210
Val	Leu	Ser	Gln	Lys	Arg	Cys	Glu	Asp	Ala	Tyr	Pro	Arg	Gln	Ile
			215						220					225
Asp	Asp	Thr	Met	Phe	Cys	Ala	Gly	Asp	Lys	Ala	Gly	Arg	Asp	Ser
			230						235					240
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Val	Val	Cys	Asn	Gly	Ser	Leu
			245						250					255
Gln	Gly	Leu	Val	Ser	Trp	Gly	Asp	Tyr	Pro	Cys	Ala	Arg	Pro	Asn
			260						265					270
Arg	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Lys	Trp	Ile
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Gln	Glu	Thr	Ile	Gln	Ala	Asn	Ser							

<210> 310
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 310
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<210> 311
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 311
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<210> 312
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 313
 <211> 3010
 <212> DNA
 <213> Homo sapiens

<400> 313
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 gctcttggtt ttctgggctg gggcctaggc agggctggga tgaggcttgt 2300
 acaaccccca ccaccaattt ccaggggact ccagggtcct gaggcctccc 2350
 aggagggcct tgggggtgat gaccoccttc ctgaggtggc tgtctccatg 2400
 aggaggccaa cccttgccat tgaccgtggc cacttgagcc caggccaggc 2450
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 ggtcgggggg actggggcac cagaccaggc accacctgga cactttcttg 2550
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 cagggttgga gccgggtcct cagctgtctg ctcagcagcc ctggacccgc 2700
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 ctctcctcgg gcaggagggg aggtggcttc ctccaaagga caccgatgg 2850
 cagggtgccta gggggtgtgg ggttcgcttc tcccttcccc tccactgaa 2900
 gtttgtgctt aaaaaacaat aaatttgact tggcaccact gggggttgg 2950
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 acatgcgcag 3010

<210> 314
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 314
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 Val Leu Cys Thr Val Leu Leu Ala Leu Ala Val Leu Leu Ala Val
 35 40 45
 Ala Val Thr Gly Ala Val Leu Phe Leu Asn His Ala His Ala Pro
 50 55 60
 Gly Thr Ala Pro Pro Pro Val Val Ser Thr Gly Ala Ala Ser Ala
 65 70 75
 Asn Ser Ala Leu Val Thr Val Glu Arg Ala Asp Ser Ser His Leu
 80 85 90
 Ser Ile Leu Ile Asp Pro Arg Cys Pro Asp Leu Thr Asp Ser Phe
 95 100 105

Ala	Arg	Leu	Glu	Ser	Ala	Gln	Ala	Ser	Val	Leu	Gln	Ala	Leu	Thr
				110					115					120
Glu	His	Gln	Ala	Gln	Pro	Arg	Leu	Val	Gly	Asp	Gln	Glu	Gln	Glu
				125					130					135
Leu	Leu	Asp	Thr	Leu	Ala	Asp	Gln	Leu	Pro	Arg	Leu	Leu	Ala	Arg
				140					145					150
Ala	Ser	Glu	Leu	Gln	Thr	Glu	Cys	Met	Gly	Leu	Arg	Lys	Gly	His
				155					160					165
Gly	Thr	Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Gln	Ser	Glu	Gln	Gly
				170					175					180
Arg	Leu	Ile	Gln	Leu	Leu	Ser	Glu	Ser	Gln	Gly	His	Met	Ala	His
				185					190					195
Leu	Val	Asn	Ser	Val	Ser	Asp	Ile	Leu	Asp	Ala	Leu	Gln	Arg	Asp
				200					205					210
Arg	Gly	Leu	Gly	Arg	Pro	Arg	Asn	Lys	Ala	Asp	Leu	Gln	Arg	Ala
				215					220					225
Pro	Ala	Arg	Gly	Thr	Arg	Pro	Arg	Gly	Cys	Ala	Thr	Gly	Ser	Arg
				230					235					240
Pro	Arg	Asp	Cys	Leu	Asp	Val	Leu	Leu	Ser	Gly	Gln	Gln	Asp	Asp
				245					250					255
Gly	Val	Tyr	Ser	Val	Phe	Pro	Thr	His	Tyr	Pro	Ala	Gly	Phe	Gln
				260					265					270
Val	Tyr	Cys	Asp	Met	Arg	Thr	Asp	Gly	Gly	Gly	Trp	Thr	Val	Phe
				275					280					285
Gln	Arg	Arg	Glu	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Gly	Trp	Asp
				290					295					300
Ala	Tyr	Arg	Asp	Gly	Phe	Gly	Arg	Leu	Thr	Gly	Glu	His	Trp	Leu
				305					310					315
Gly	Leu	Lys	Arg	Ile	His	Ala	Leu	Thr	Thr	Gln	Ala	Ala	Tyr	Glu
				320					325					330
Leu	His	Val	Asp	Leu	Glu	Asp	Phe	Glu	Asn	Gly	Thr	Ala	Tyr	Ala
				335					340					345
Arg	Tyr	Gly	Ser	Phe	Gly	Val	Gly	Leu	Phe	Ser	Val	Asp	Pro	Glu
				350					355					360
Glu	Asp	Gly	Tyr	Pro	Leu	Thr	Val	Ala	Asp	Tyr	Ser	Gly	Thr	Ala
				365					370					375
Gly	Asp	Ser	Leu	Leu	Lys	His	Ser	Gly	Met	Arg	Phe	Thr	Thr	Lys
				380					385					390
Asp	Arg	Asp	Ser	Asp	His	Ser	Glu	Asn	Asn	Cys	Ala	Ala	Phe	Tyr
				395					400					405
Arg	Gly	Ala	Trp	Trp	Tyr	Arg	Asn	Cys	His	Thr	Ser	Asn	Leu	Asn
				410					415					420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
 425 430
 Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
 440 445 450
 Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
 455 460

<210> 315
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 315
 cacacgtcca acctcaatgg gcag 24

<210> 316
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 316
 gaccagcagg gccaaaggaca agg 23

<210> 317
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 317
 gtctctgtgag atgaagatcc ggccgggtccg ggagtaccgc ttag 44

<210> 318
 <211> 1841
 <212> DNA
 <213> Homo sapiens

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 ccaagtacag cagcagcagg gacatgctg atgatgatgg ggacaccacc 200
 atgagcctgc atttcaagc ctctgccaca actcggcacc cagagccccg 250
 gcgcacagag cacagggctc cctcttcaac gtggcgacca gtggccctga 300
 ccctgctgac tttgtgcttg gtgctgctga tagggctggc agccctgggg 350
 cttttgtttt ttacagtacta ccagctctcc aatactggtc aagacccatc 400

ttctcaaatg gaagaaagat taggaaatac gtcccaagag ttgcaatctc 450
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 tctaccatgc tgaagataaa caaacaagaa gacctggaat ttgcccgcgtc 700
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 tgtggccatc ctcaatggga tgatcttctc aaaggactgc aaagaattga 900
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 catgtccccc ctgaaacatt aggcgaaggt gactgattcg cctctgcaa 1000
 ctacaaatag cagagtgcgc caggcgtgtc caaagcaagg gctagttgag 1050
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 aaaatgggtt ctctgttttc ctgttcagga taccagcat tctgagctt 1150
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 actgaagatt taataataat aaatgtaaat actgtgaaaa a 1841

<210> 319

<211> 280

<212> FRT

<213> Homo sapiens

<400> 319

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Gly	Asp	Thr	Thr	Met	Ser	Leu	His	Ser	Gln	Ala	Ser	Ala	Thr	Thr
				20					25					30
Arg	His	Pro	Glu	Pro	Arg	Arg	Thr	Glu	His	Arg	Ala	Pro	Ser	Ser
				35					40					45
Thr	Trp	Arg	Pro	Val	Ala	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Leu	Val
				50					55					60
Leu	Leu	Ile	Gly	Leu	Ala	Ala	Leu	Gly	Leu	Phe	Phe	Gln	Tyr	
				65					70					75
Tyr	Gln	Leu	Ser	Asn	Thr	Gly	Gln	Asp	Thr	Ile	Ser	Gln	Met	Glu
				80					85					90
Glu	Arg	Leu	Gly	Asn	Thr	Ser	Gln	Glu	Leu	Gln	Ser	Leu	Gln	Val
				95					100					105
Gln	Asn	Ile	Lys	Leu	Ala	Gly	Ser	Leu	Gln	His	Val	Ala	Glu	Lys
				110					115					120
Leu	Cys	Arg	Glu	Leu	Tyr	Asn	Lys	Ala	Gly	Ala	His	Arg	Cys	Ser
				125					130					135
Pro	Cys	Thr	Glu	Gln	Trp	Lys	Trp	His	Gly	Asp	Asn	Cys	Tyr	Gln
				140					145					150
Phe	Tyr	Lys	Asp	Ser	Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys
				155					160					165
Leu	Ser	Glu	Asn	Ser	Thr	Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp
				170					175					180
Leu	Glu	Phe	Ala	Ala	Ser	Gln	Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser
				185					190					195
Tyr	Trp	Thr	Gly	Leu	Leu	Arg	Pro	Asp	Ser	Gly	Lys	Ala	Trp	Leu
				200					205					210
Trp	Met	Asp	Gly	Thr	Pro	Phe	Thr	Ser	Glu	Leu	Phe	His	Ile	Ile
				215					220					225
Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	Asp	Cys	Val	Ala	Ile	Leu
				230					235					240
Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	Glu	Leu	Lys	Arg	Cys
				245					250					255
Val	Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	Glu	Ser	Leu	His
				260					265					270
Val	Pro	Pro	Glu	Thr	Leu	Gly	Glu	Gly	Asp					
				275					280					

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

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<220>
<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
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gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100
cttttgcac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200
ggtgctgctg atagggtctg cagccctggg gcttttgttt tttcagtact 250
accagctctc caatactggt caagacacca tttctcaaat ggaagaaaaga 300
ttaggaaata cgtccaaga gttgcaatnt nttaagttcc agaataataa 350
gcttgacgga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400
ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450
atacacacac cacttccc 468

<210> 321
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 321
atgcaggcca agtacagcag cac 23

<210> 322
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 322
catgctgacg acttctctga agc 23

<210> 323
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc tctgcttctt ggg 23

<210> 324
<211> 40
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 324
atgctggatg atgatgggga caccacatg agcctgcatt 40

<210> 325
<211> 2988
<212> DNA
<213> Homo sapiens

<400> 325
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gagggagcgg gcccgccgcg ggggcccag cctccggat ccgcccctc 150
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ggcgcgccgg cccaactcgg tgcagcccg agcggagcgc gagaagccc 450
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caccctgcac agcccgcca gcccgccaaa aaggccgtca ggaccgccta 550
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<210> 326
<211> 775
<212> PRT
<213> Homo sapiens

<400> 326
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Val Thr Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro
35 40 45
Gly Asp Ser Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg
50 55 60
Arg Pro Asn Ser Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly
65 70 75
Ala Gly Glu Gly Ala Gly Glu Asn Trp Glu Pro Arg Val Leu Pro
80 85 90
Tyr His Pro Ala Gln Pro Gly Gln Ala Ala Lys Lys Ala Val Arg
95 100 105
Thr Arg Tyr Ile Ser Thr Glu Leu Gly Ile Arg Gln Arg Leu Leu
110 115 120
Val Ala Val Leu Thr Ser Gln Thr Thr Leu Pro Thr Leu Gly Val
125 130 135
Ala Val Asn Arg Thr Leu Gly His Arg Leu Glu Arg Val Val Phe
140 145 150
Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro Gly Met Ala Val
155 160 165
Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His Leu His Leu Ala
170 175 180
Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe Asp Trp Phe
185 190 195
Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly Leu Ala
200 205 210
Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu Tyr
215 220 225
Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
230 235 240
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu
245 250 255
Leu Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile
260 265 270

Val Ser Ala Arg	Pro Asp Glu Trp Leu	Gly Arg Cys Ile Leu	Asp
275		280	285
Ala Thr Gly Val	Gly Cys Thr Gly Asp	His Glu Gly Val His	Tyr
290		295	300
Ser His Leu Glu	Leu Ser Pro Gly Glu	Pro Val Gln Glu Gly	Asp
305		310	315
Pro His Phe Arg	Ser Ala Leu Thr Ala	His Pro Val Arg Asp	Pro
320		325	330
Val His Met Tyr	Gln Leu His Lys Ala	Phe Ala Arg Ala Glu	Leu
335		340	345
Glu Arg Thr Tyr	Gln Glu Ile Gln Glu	Leu Gln Trp Glu Ile	Gln
350		355	360
Asn Thr Ser His	Leu Ala Val Asp Gly	Asp Arg Ala Ala Ala	Trp
365		370	375
Pro Val Gly Ile	Pro Ala Pro Ser Arg	Pro Ala Ser Arg Phe	Glu
380		385	390
Val Leu Arg Trp	Asp Tyr Phe Thr Glu	Gln His Ala Phe Ser	Cys
395		400	405
Ala Asp Gly Ser	Pro Arg Cys Pro Leu	Arg Gly Ala Asp Arg	Ala
410		415	420
Asp Val Ala Asp	Val Leu Gly Thr Ala	Leu Glu Glu Leu Asn	Arg
425		430	435
Arg Tyr His Pro	Ala Leu Arg Leu Gln	Lys Gln Gln Leu Val	Asn
440		445	450
Gly Tyr Arg Arg	Phe Asp Pro Ala Arg	Gly Met Glu Tyr Thr	Leu
455		460	465
Asp Leu Gln Leu	Glu Ala Leu Thr Pro	Gln Gly Gly Arg Arg	Pro
470		475	480
Leu Thr Arg Arg	Val Gln Leu Leu Arg	Pro Leu Ser Arg Val	Glu
485		490	495
Ile Leu Pro Val	Pro Tyr Val Thr Glu	Ala Ser Arg Leu Thr	Val
500		505	510
Leu Leu Pro Leu	Ala Ala Ala Glu Arg	Asp Leu Ala Pro Gly	Phe
515		520	525
Leu Glu Ala Phe	Ala Thr Ala Ala Leu	Glu Pro Gly Asp Ala	Ala
530		535	540
Ala Ala Leu Thr	Leu Leu Leu Leu Tyr	Glu Pro Arg Gln Ala	Gln
545		550	555
Arg Val Ala His	Ala Asp Val Phe Ala	Pro Val Lys Ala His	Val
560		565	570
Ala Glu Leu Glu	Arg Arg Phe Pro Gly	Ala Arg Val Pro Trp	Leu
575		580	585

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 tgacctcttc tcagagcacc taattaaag ggctgaaagt ctgaa 1095

<210> 334
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 334
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 20 25 30
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly
 35 40 45
 Lys Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu
 50 55 60
 Pro Glu Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly
 65 70 75
 Tyr Asp Lys Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val
 80 85 90
 Phe Phe Phe Gly Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe
 95 100 105
 Val Ala Tyr Leu Pro Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg
 110 115 120
 Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro
 125 130 135
 Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
 140 145 150

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aggactgttg tcgccccgtc cgctgtggcg ggaaagcgcc ccccgagaacc 150
gaccacacgg tggaagagg acccagaacc cgaggacgaa aactgtgatg 200
agaagaacc agactcccat ggttatgaca aggacccctt ttggacgtc 250
tggaacatgc gaattgtctt ctctctttgc gtctccatca tctgtgtctc 300
tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtggg 350
ccgcgccgca agctgagagg cttgtgaaat accgagaggg caatggcctt 400
cccatcatgg aatccaactg cttgcacccc agcaagatcc ag 442
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<220>
<223> Synthetic oligonucleotide probe

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<210> 337
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 337
ggtgcttctt gagccccact tagc 24

<220>
<223> Synthetic oligonucleotide probe

<210>	339
<211>	2162
<212>	DNA

0609

295

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 tgggtggcgt gtgctacggc tccttctaca atctcctcac ccgaaccttc 1650
 cacatcgagg agccccgcac aggtggcctg gccaaagcgc tggccaacct 1700
 tatccggcgc gcccgaggtg tcccccaact ctgattcttg ccctttccag 1750
 cagctgcagc tgccgtttct ctctggggag gggagcccaa gggctgtttc 1800
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 aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900
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 ggccacctct atattgaggt gctcaataag caaaagtggc cgggtggctgc 2000
 tgtattggac agcacagaaa aagatttcca tcaccacaga aaggtcggct 2050
 ggcagcactg gccaaagtga tgggggtgtc tacacagtgt atgtcactgt 2100
 gtagtggatg gagtttactg tttgtggaat aaaaacggct gtttccgtgg 2150
 aaaaaaaaaa aa 2162

<210> 340
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Pro Leu Ala Leu Leu Val Leu Leu Leu Gly Pro Gly Gly
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 20 25 30
 Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln
 35 40 45
 Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser
 50 55 60
 His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys
 65 70 75
 Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
 80 85 90
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly
 95 100 105
 Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp
 110 115 120
 Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys
 125 130 135
 Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr
 140 145 150

Ala Ser Phe Lys	Pro Leu Gly Leu Ala	Asn Asp Thr Asp His Tyr
155	160	165
Phe Leu Arg Tyr	Ala Val Leu Pro Arg	Glu Val Val Cys Thr Glu
170	175	180
Asn Leu Thr Pro	Trp Lys Lys Leu Leu	Pro Cys Ser Ser Lys Ala
185	190	195
Gly Leu Ser Val	Leu Leu Lys Ala Asp	Arg Leu Phe His Thr Ser
200	205	210
Tyr His Ser Gln	Ala Val His Ile Arg	Pro Val Cys Arg Asn Ala
215	220	225
Arg Cys Thr Ser	Ile Ser Trp Glu Leu Arg	Gln Thr Leu Ser Val
230	235	240
Val Phe Asp Ala	Phe Ile Thr Gly Gln	Gly Lys Lys Asp Trp Ser
245	250	255
Leu Phe Arg Met	Phe Ser Arg Thr Leu	Thr Glu Pro Cys Pro Leu
260	265	270
Ala Ser Glu Ser	Arg Val Tyr Val Asp	Ile Thr Thr Tyr Asn Gln
275	280	285
Asp Asn Glu Thr	Leu Glu Val His Pro	Pro Pro Thr Thr Thr Tyr
290	295	300
Gln Asp Val Ile	Leu Gly Thr Arg Lys	Thr Tyr Ala Ile Tyr Asp
305	310	315
Leu Leu Asp Thr	Ala Met Ile Asn Asn	Ser Arg Asn Leu Asn Ile
320	325	330
Gln Leu Lys Trp	Lys Arg Pro Pro Glu	Asn Glu Ala Pro Pro Val
335	340	345
Pro Phe Leu His	Ala Gln Arg Tyr Val	Ser Gly Tyr Gly Leu Gln
350	355	360
Lys Gly Glu Leu	Ser Thr Leu Leu Tyr	Asn Thr His Pro Tyr Arg
365	370	375
Ala Phe Pro Val	Leu Leu Leu Asp Thr	Val Pro Trp Tyr Leu Arg
380	385	390
Leu Tyr Val His	Thr Leu Thr Ile Thr	Ser Lys Gly Lys Glu Asn
395	400	405
Lys Pro Ser Tyr	Ile His Tyr Gln Pro	Ala Gln Asp Arg Leu Gln
410	415	420
Pro His Leu Leu	Glu Met Leu Ile Gln	Leu Pro Ala Asn Ser Val
425	430	435
Thr Lys Val Ser	Ile Gln Phe Glu Arg	Ala Leu Leu Lys Trp Thr
440	445	450
Glu Tyr Thr Pro	Asp Pro Asn His Gly	Phe Tyr Val Ser Pro Ser
455	460	465

<400> 344
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 gtttgccag ctgacaacgt acgctgcttc aagtcogatc ctccccagtg 150
 tcacacagac caggactgtc tgggggaaaag gaagtgtgtg tacctgcact 200
 gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250
 aaggatgaag atgtgtcaag gccataacct gagccaggat gggaggccaa 300
 gtgtccaggc tctctcteta ccaggtgtcc tcagaaatga tgctgggtcc 350
 tttctacctc tgggggtcac tctcacttgg cacctgcccc tgagggtcct 400
 gagacttga atattgaaga agcaataccc aacccccca aagaaaacct 450
 gagcttgaag tctttttccc caaaaagagg gaagagtccac aaaaagtcca 500
 gaccccgagg acggtacttt cctctctac ctggtgctcc tcctaatagc 550
 tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600
 aaagagctgc ctggcccttc tgcaatgtgt gatcacagct agaaggcact 650
 gtcagagaag agaaactggt cctcaccaga tgctgaatct gctggtgctc 700
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 tttataatcc aa 762

<210> 345
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 345
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 20 25 30
 Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
 35 40 45
 Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
 50 55 60
 Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
 65 70 75
 Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
 80 85 90
 Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
 95 100 105
 Thr Arg Cys Pro Gln Lys
 110

<210> 346
 <211> 2528
 <212> DNA
 <213> Homo sapiens

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 gccccaggac atgcagaacc ttctctctaga acccgaccca ccaccatgag 150
 gtctctgcctg tggagatgca ggcacctgag ccaaggcgtc cagtggctct 200
 tgcttctggc tgtctctggc ttctttctct tgccttgcc ctcttttatt 250
 aaggagcctc aaacaaagcc ttccaggcat caacgcacag agaacattaa 300
 agaaaggctc ctacagtccc tggcaaagcc taagtcccag gacccacaa 350
 gggcgaggag gacaaccatc tatgcagagc cagcgccaga gaacaatgcc 400
 ctcaacacac aaaccagacc caaggccac accaccggag acagaggaaa 450
 ggagggcaac caggcaccgc cggaggagca ggacaagggt cccacacag 500
 cacagagggc agcatggaag agcccagaaa aagagaaaac catggtgaac 550
 aactgtctac ccagaggcca agatgcaggg atggcctctg gcaggacaga 600
 ggcacaatca tggaaagacc aggcacacaa gacgacccaa ggaatgggg 650
 gccagaccag gaagctgacg gcctccagga cgggtgtcaga gaagcaccag 700
 ggcaaagcgg caaccacagc caagacgctc attccaaaa gtcagcacag 750
 aatgtctggc cccacaggag cagtgtcaac aaggacgaga cagaaaggag 800
 tgaccacagc agtcatccca cctaaggaga agaaacctca ggccaccca 850
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 aacactttgc accaccctt ggcttcatgg agctcaacta ctcttgggtg 1150
 cagaaggctg tgacacgctt cctccagtgc cccagcagc agctgtctct 1200
 ggccagcctc cccgtggga gccctcgtg catcacctgt gccgtgtgtg 1250
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 cagcactacg tgttccgatt gagcggagct ctcatataag gctacgaaca 1350
 ggatgtgggg actcggacat ccttctacgg ctttacgcc ttctccctga 1400
 cccagtcact ccttatattg ggcaatcggg gtttcaagaa cgtgcctctt 1450

gggaaggacg tccgctactt gcacttccctg gaaggcaccg gggactatga 1500
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 gacaggtacc tgttgctgca cccagacttt ctccgataca tgaagaacag 1650
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 gtgagtgcct atggcttcat cactgagggc catgagcgct tttctgatca 1800
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 tcaagctgga gagagaagtc tggaagcggc tacacgatga agggataatc 1900
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 ctcaagatgg caaatggcta attgaggttc tgaagttctt cagtacattg 2150
 ctgtaggtcc tgaggccagg gatttttaat taaatggggt gatgggtggc 2200
 caataccaca attcctgctg aaaaacactc ttccagtcca aaagcttctt 2250
 gatacagaaa aaagagcctg gatttacaga aacatataga tctggtttga 2300
 attccagatc gagtttacag ttgtgaaatc ttgaaggatc tacttaactt 2350
 cactacagat tgtctagaag acctttctag gagttatctg attctagaag 2400
 ggtctatact tgtccttgct ttttaagctat ttgacaactc tacgtgttgc 2450
 agaaaaactga taataatata aatgattgtt gtccatggaa aggcataata 2500
 attttctaca gtgaaaaaaaa aaaaaaaaaa 2528

<210> 347
 <211> 600
 <212> PRT
 <213> Homo sapiens

<400> 347
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 Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala
 20 25 30
 Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His
 35 40 45
 Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala
 50 55 60
 Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

	65		70		75
Tyr Ala Glu Pro	Ala 80	Pro Glu Asn Asn	Ala 85	Leu Asn Thr Gln	Thr 90
Gln Pro Lys Ala	His 95	Thr Thr Gly Asp	Arg 100	Gly Lys Glu Ala	Asn 105
Gln Ala Pro Pro	Glu 110	Glu Gln Asp Lys	Val 115	Pro His Thr Ala	Gln 120
Arg Ala Ala Trp	Lys 125	Ser Pro Glu Lys	Glu 130	Lys Thr Met Val	Asn 135
Thr Leu Ser Pro	Arg 140	Gly Gln Asp Ala	Gly 145	Met Ala Ser Gly	Arg 150
Thr Glu Ala Gln	Ser 155	Trp Lys Ser Gln	Asp 160	Thr Lys Thr Thr	Gln 165
Gly Asn Gly Gly	Gln 170	Thr Arg Lys Leu	Thr 175	Ala Ser Arg Thr	Val 180
Ser Glu Lys His	Gln 185	Gly Lys Ala Ala	Thr 190	Thr Ala Lys Thr	Leu 195
Ile Pro Lys Ser	Gln 200	His Arg Met Leu	Ala 205	Pro Thr Gly Ala	Val 210
Ser Thr Arg Thr	Arg 215	Gln Lys Gly Val	Thr 220	Thr Ala Val Ile	Pro 225
Pro Lys Glu Lys	Lys 230	Pro Gln Ala Thr	Pro 235	Pro Pro Ala Pro	Phe 240
Gln Ser Pro Thr	Thr 245	Gln Arg Asn Gln	Arg 250	Leu Lys Ala Ala	Asn 255
Phe Lys Ser Glu	Pro 260	Arg Trp Asp Phe	Glu 265	Glu Lys Tyr Ser	Phe 270
Glu Ile Gly Gly	Leu 275	Gln Thr Thr Cys	Pro 280	Asp Ser Val Lys	Ile 285
Lys Ala Ser Lys	Ser 290	Leu Trp Leu Gln	Lys 295	Leu Phe Leu Pro	Asn 300
Leu Thr Leu Phe	Leu 305	Asp Ser Arg His	Phe 310	Asn Gln Ser Glu	Trp 315
Asp Arg Leu Glu	His 320	Phe Ala Pro Pro	Phe 325	Gly Phe Met Glu	Leu 330
Asn Tyr Ser Leu	Val 335	Gln Lys Val Val	Thr 340	Arg Phe Pro Pro	Val 345
Pro Gln Gln Gln	Leu 350	Leu Leu Ala Ser	Leu 355	Pro Ala Gly Ser	Leu 360
Arg Cys Ile Thr	Cys 365	Ala Val Val Gly	Asn 370	Gly Gly Ile Leu	Asn 375
Asn Ser His Met	Gly 380	Gln Glu Ile Asp	Ser 385	His Asp Tyr Val	Phe 390

380	385	390
Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly		
395	400	405
Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln		
410	415	420
Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn Val Pro Leu		
425	430	435
Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asp		
440	445	450
Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met Ser		
455	460	465
Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg		
470	475	480
Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe		
485	490	495
Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp		
500	505	510
Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu		
515	520	525
Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly		
530	535	540
Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp		
545	550	555
Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys		
560	565	570
Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile		
575	580	585
Arg Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn		
590	595	600

<210> 348
 <211> 496
 <212> DNA
 <213> Homo sapiens

<400> 348
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 gaaggacaag tttctaaaac accttacagg cctcttttat tttagtccaa 150
 agtgcagcaa acacttccat agactttatc acāacaccag agactgcacc 200
 attcctgcac actataaaag atgcgccagg cttcttaccg ggctggctgt 250
 cagtccagtg tgcattggagg ataagtgagc agaccgtaca ggagcagcac 300
 accaggagcc atgagaagtg ccttggaaac caacagggaa acagaactat 350

atctacccca gctgggcccc cagtctacaa ccctgcagct cctcctccct 650
 atatgccacc acagccctct taccggggag cctgaggaac cagccatgtc 700
 tctgtgccc ctctcagtgat gccaaccttg ggagatgccc tcactcctgta 750
 cctgcatctg gtcctggggg tggcaggagt cctccagcca ccaggcccca 800
 gaccaagcca agccctgggc cctactgggg acagagcccc agggaaagtgg 850
 aacaggagct gaactagaac tatgaggggt tggggggagg gcttggaatt 900
 atgggctatt ttactgggg gcaaggagg gagatgacag cctgggtcac 950
 agtgctgtt ttcaaatagt cctctctgtc ccaagatccc agccaggaag 1000
 gctggggccc tactgtttgt cccctctggg ctgggggtggg gggaggagg 1050
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<210> 351

<211> 197

<212> PRT

<213> Homo sapiens

<400> 351

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				20					25					30
Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe
				35					40					45
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg
				50					55					60
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln
				65					70					75
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala
				80					85					90
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys
				95					100					105
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln
				110					115					120
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile
				125					130					135
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly
				140					145					150
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro
				155					160					165
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn
				170					175					180

Pro Ala Ala Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
185 190 195

Gly Ala

<210> 352
<211> 3226
<212> DNA
<213> Homo sapiens

<400> 352
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ctcaaatggt cccctgcaac catgtcattt ctactttcct cactgttgge 150
tctcttaact gtgtccactc ctctcatggtg tcagagcact gaagcatctc 200
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cacgctgacc ttctggggaa ccacgaaagt agaaatcaca gccagtcagc 350
ccaccagcac catcatcctg catagtcacc acctgcagat atctagggcc 400
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ctgtgaagat gagcacctat ctggtggcct tcatcatttc agattttgag 850
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caagatcttg ctgctattcc cgactttcag tctggtgcta tggaaaactg 1050
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cttctgcac aagtaagctt ggcatcacag tgactgtggc ccatgaactg 1150
gccaccaggt ggtttgggaa cctggtcact atggaatggt ggaatgatct 1200
ttggctaagt gaaggatttg ccaaatttat ggagttttgt tctgtcagtg 1250
tgacccatcc tgaactgaaa gttggagatt atttcttttg caaatgtttt 1300

gacgcaatgg aggtagatgc tttaaattcc tcacacccctg tgtctacacc 1350
 tgttgaaat cctgctcaga tccgggagat gtttgatgat gtttcttatg 1400
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 gcatttaaaa gtggatttgt acagtatctc cagaagcata gctataaaaa 1500
 tacaaaaaac gaggacctgt gggatagtat ggcaagtatt tgccctacag 1550
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 ggctattaca ttgtgcatta cgaggatgat ggatgggact ctttgactgg 1950
 ccttttaaaa ggaacacaca cagcagtcag cagtaatgat cgggcaagtc 2000
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 cgtgtttcaa ggtttgaatg agctgattcc tatgtataag ttaatggaga 2150
 aaagagatat gaatgaagtg gaaactcaat tcaaggcctt cctcatcagg 2200
 ctgctaaggg acctcattga taagcagaca tggacagacg agggctcagt 2250
 ctcagagcaa atgctgcgga gtgaactact actcctcgcc tgtgtgcaca 2300
 actatcagcc gtgcgtacag agggcagaag gctatttcag aaagtggaa 2350
 gaatccaatg gaaacttgag cctgcctgtc gacgtgacct tggcagtgtt 2400
 tgctgtgggg gccagagca cagaaggctg ggattttctt tatagtaaat 2450
 atcagtttct tttgtccagt actgagaaaa gccaaattga atttgcctc 2500
 tgcgaaccc aaaataagga aaagcttcaa tggctactag atgaaagctt 2550
 taaggagat aaaataaaaa ctcaggagtt tccacaaatt cttacactca 2600
 ttgacaggaa ccagtagga taccactgg cctggcaatt totgagaaa 2650
 aactgaaca aacttgata aaagtttgaa cttggctcat cttcatagc 2700
 ccacatggta atgggtacaa caaatcaatt ctccacaaga acacggcttg 2750
 aagaggtaaa aggattcttc agctcttga aagaaaaatg ttctcagctc 2800
 cgttgtgtcc aacagacaat tgaaccatt gaagaaaaca tcggttgat 2850
 ggataagaat ttgataaaa tcagagtgtg gctgcaaagt gaaaagcttg 2900

aacgtatgta aaaattcctc ccttgcccg ttcctgttat ctctaatac 2950
 caacattttg ttgagtgtat tttcaaacta gagatggctg ttttggctcc 3000
 aactggagat acttttttcc cttcaactca ttttttgact atocctgtga 3050
 aaagaatagc tgtagtttt tcatgaatgg gctttttcat gaatgggcta 3100
 tcgctacat gtgttttgtt catcacaggt gttgccctgc aacgtaaacc 3150
 caagtgttg gttccctgcc acagaagaat aaagtacctt attcttctca 3200
 aaaaaaaaa aaaaaaaaa aaaaaa 3226

<210> 353
 <211> 941
 <212> PRT
 <213> Homo sapiens

<400> 353
 Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe
 1 5 10 15
 Leu Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser
 20 25 30
 Trp Cys Gln Ser Thr Glu Ala Ser Pro Lys Arg Ser Asp Gly Thr
 35 40 45
 Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile Pro
 50 55 60
 Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr
 65 70 75
 Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr
 80 85 90
 Ser Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala
 95 100 105
 Thr Leu Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu
 110 115 120
 Gln Val Leu Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala
 125 130 135
 Pro Glu Pro Leu Leu Val Gly Leu Pro Tyr Thr Val Val Ile His
 140 145 150
 Tyr Ala Gly Asn Leu Ser Glu Thr Phe His Gly Phe Tyr Lys Ser
 155 160 165
 Thr Tyr Arg Thr Lys Glu Gly Glu Leu Arg Ile Leu Ala Ser Thr
 170 175 180
 Gln Phe Glu Pro Thr Ala Ala Arg Met Ala Phe Pro Cys Phe Asp
 185 190 195
 Glu Pro Ala Phe Lys Ala Ser Phe Ser Ile Lys Ile Arg Arg Glu
 200 205 210
 Pro Arg His Leu Ala Ile Ser Asn Met Pro Leu Val Lys Ser Val

215	220	225
Thr Val Ala Glu Gly Leu Ile Glu Asp	His Phe Asp Val Thr Val	230
230	235	240
Lys Met Ser Thr Tyr Leu Val Ala Phe	Ile Ile Ser Asp Phe Glu	245
245	250	255
Ser Val Ser Lys Ile Thr Lys Ser Gly	Val Lys Val Ser Val Tyr	260
260	265	270
Ala Val Pro Asp Lys Ile Asn Gln Ala	Asp Tyr Ala Leu Asp Ala	275
275	280	285
Ala Val Thr Leu Leu Glu Phe Tyr Glu	Asp Tyr Phe Ser Ile Pro	290
290	295	300
Tyr Pro Leu Pro Lys Gln Asp Leu Ala	Ala Ile Pro Asp Phe Gln	305
305	310	315
Ser Gly Ala Met Glu Asn Trp Gly Leu	Thr Thr Tyr Arg Glu Ser	320
320	325	330
Ala Leu Leu Phe Asp Ala Glu Lys Ser	Ser Ala Ser Ser Lys Leu	335
335	340	345
Gly Ile Thr Val Thr Val Ala His Glu	Leu Ala His Gln Trp Phe	350
350	355	360
Gly Asn Leu Val Thr Met Glu Trp Trp	Asn Asp Leu Trp Leu Asn	365
365	370	375
Glu Gly Phe Ala Lys Phe Met Glu Phe	Val Ser Val Ser Val Thr	380
380	385	390
His Pro Glu Leu Lys Val Gly Asp Tyr	Phe Phe Gly Lys Cys Phe	395
395	400	405
Asp Ala Met Glu Val Asp Ala Leu Asn	Ser Ser His Pro Val Ser	410
410	415	420
Thr Pro Val Glu Asn Pro Ala Gln Ile	Arg Glu Met Phe Asp Asp	425
425	430	435
Val Ser Tyr Asp Lys Gly Ala Cys Ile	Leu Asn Met Leu Arg Glu	440
440	445	450
Tyr Leu Ser Ala Asp Ala Phe Lys Ser	Gly Ile Val Gln Tyr Leu	455
455	460	465
Gln Lys His Ser Tyr Lys Asn Thr Lys	Asn Glu Asp Leu Trp Asp	470
470	475	480
Ser Met Ala Ser Ile Cys Pro Thr Asp	Gly Val Lys Gly Met Asp	485
485	490	495
Gly Phe Cys Ser Arg Ser Gln His Ser	Ser Ser Ser Ser His Trp	500
500	505	510
His Gln Glu Gly Val Asp Val Lys Thr	Met Met Asn Thr Trp Thr	515
515	520	525
Leu Gln Arg Gly Phe Pro Leu Ile Thr	Ile Thr Val Arg Gly Arg	

530	535	540
Asn Val His Met Lys Gln Glu His Tyr	Met Lys Gly Ser Asp Gly	
545	550	555
Ala Pro Asp Thr Gly Tyr Leu Trp His	Val Pro Leu Thr Phe Ile	
560	565	570
Thr Ser Lys Ser Asn Met Val His Arg	Phe Leu Leu Lys Thr Lys	
575	580	585
Thr Asp Val Leu Ile Leu Pro Glu Glu	Val Glu Trp Ile Lys Phe	
590	595	600
Asn Val Gly Met Asn Gly Tyr Tyr Ile	Val His Tyr Glu Asp Asp	
605	610	615
Gly Trp Asp Ser Leu Thr Gly Leu Leu	Lys Gly Thr His Thr Ala	
620	625	630
Val Ser Ser Asn Asp Arg Ala Ser Leu	Ile Asn Asn Ala Phe Gln	
635	640	645
Leu Val Ser Ile Gly Lys Leu Ser Ile	Glu Lys Ala Leu Asp Leu	
650	655	660
Ser Leu Tyr Leu Lys His Glu Thr Glu	Ile Met Pro Val Phe Gln	
665	670	675
Gly Leu Asn Glu Leu Ile Pro Met Tyr	Lys Leu Met Glu Lys Arg	
680	685	690
Asp Met Asn Glu Val Glu Thr Gln Phe	Lys Ala Phe Leu Ile Arg	
695	700	705
Leu Leu Arg Asp Leu Ile Asp Lys Gln	Thr Trp Thr Asp Glu Gly	
710	715	720
Ser Val Ser Glu Gln Met Leu Arg Ser	Glu Leu Leu Leu Leu Ala	
725	730	735
Cys Val His Asn Tyr Gln Pro Cys Val	Gln Arg Ala Glu Gly Tyr	
740	745	750
Phe Arg Lys Trp Lys Glu Ser Asn Gly	Asn Leu Ser Leu Pro Val	
755	760	765
Asp Val Thr Leu Ala Val Phe Ala Val	Gly Ala Gln Ser Thr Glu	
770	775	780
Gly Trp Asp Phe Leu Tyr Ser Lys Tyr	Gln Phe Ser Leu Ser Ser	
785	790	795
Thr Glu Lys Ser Gln Ile Glu Phe Ala	Leu Cys Arg Thr Gln Asn	
800	805	810
Lys Glu Lys Leu Gln Trp Leu Leu Asp	Glu Ser Phe Lys Gly Asp	
815	820	825
Lys Ile Lys Thr Gln Glu Phe Pro Gln	Ile Leu Thr Leu Ile Gly	
830	835	840
Arg Asn Pro Val Gly Tyr Pro Leu Ala	Trp Gln Phe Leu Arg Lys	

845	850	855
Asn Trp Asn Lys Leu Val Gln Lys Phe	Glu Leu Gly Ser Ser Ser	870
860	865	
Ile Ala His Met Val Met Gly Thr Thr	Asn Gln Phe Ser Thr Arg	885
875	880	
Thr Arg Leu Glu Glu Val Lys Gly Phe	Phe Ser Ser Leu Lys Glu	900
890	895	
Asn Gly Ser Gln Leu Arg Cys Val Gln	Gln Thr Ile Glu Thr Ile	915
905	910	
Glu Glu Asn Ile Gly Trp Met Asp Lys	Asn Phe Asp Lys Ile Arg	930
920	925	
Val Trp Leu Gln Ser Glu Lys Leu Glu Arg Met		
935	940	

<210> 354
 <211> 1587
 <212> DNA
 <213> Homo sapiens

<400> 354
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 tcatcctccc actgccagga gtgcaggcgc tgctctgcc gtttgggaca 100
 gttcagcatg tgtggaaggt gtccgacctt ccccgcaat ggaccctaa 150
 gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200
 ttgagagcgg accccaagtg agcctgggtgc tctccaaggg ctgcacggag 250
 gccaaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300
 ctccctgac tctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350
 acctcgtaaa ctccctcccc ctttggggccc cacagcccc agcagaccca 400
 ggatccttga ggtgccagct ctgcttgtct atggaaggct gcttgagggt 450
 gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500
 tcctcaggct caggggagga ggcattctct ccaatctgag agtccaggga 550
 tgcatgcccc agccagggtg caacctgctc aatgggacac aggaaatttg 600
 gccctggggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650
 atcgggggac caccattatg acacacggaa acttggtctca agaaccaact 700
 gatttgacca catcgaatac cgagatgtgc gagtggggc aggtgtgtca 750
 ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800
 caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850
 cactcagccc ctctgggggt gcttgtggcc tctataccc acttctgtct 900
 ctcggaacctg tgcaatagtg ccagcagcag cagcgttctg ctgaactccc 950

tccctctctca agctgccccct gtcccaggag accggcagtg tcctacctgt 1000
 gtgcagcccc ttggaacctg ttcaagtggc tccccccgaa tgacctgccc 1050
 cagggggcgcc actcattgtt atgatgggtg cattcatctc tcaggagggtg 1100
 ggcgtgtccac caaaatgagc attcagggtc gcgtggccca accttccagc 1150
 ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200
 gcgtgatgtg cagcctctct cctctcagca tgagggaggt ggggctgagg 1250
 gcctggagtc tctcacttgg ggggtggggc tggcactggc cccagcgctg 1300
 tgggtggggag tggtttgcce ttctgtctaa ctctattacc cccacgattc 1350
 ttcaccgctg ctgaccaccc aactcaacc tccctctgac ctcataacct 1400
 aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450
 cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500
 gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550
 getgcatgta tctgataata cagaccctgt cctttca 1587

<210> 355
 <211> 437
 <212> PRT
 <213> Homo sapiens

<400> 355
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 Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln 30
 20 25
 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys 45
 35 40
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met 60
 50 55
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly 75
 65 70
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg 90
 80 85
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg 105
 95 100
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp 120
 110 115
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val 135
 125 130
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile 150
 140 145
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

[illegible]

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<210> 356
<211> 1238
<212> DNA
<213> Homo sapiens
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Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp	45
				35					40						
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg	60
				50					55						
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln	75
				65					70						
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser	90
				80					85						
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro	105
				95					100						
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys	120
				110					115						
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu	135
				125					130						
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu	150
				140					145						
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp	165
				155					160						
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro	180
				170					175						
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln	195
				185					190						
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys	210
				200					205						
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe	225
				215					220						
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu	240
				230					235						
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala	255
				245					250						
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn	270
				260					265						

Met

<210> 358
 <211> 972
 <212> DNA
 <213> Homo sapiens

<400> 358
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 gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100
 gttccttgat cctgccagac caccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200
 tagctcagag ctttggggct gtctgtaagg agccacagga ggaggtggtt 250
 cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300
 gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350
 gccaggctag cacagatcct aaggaatcaa catctccga gaaacgtgac 400
 atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450
 gggaagaca ggaacctttc taccttcagt gagggttcct cggccccctc 500
 atcccaatca gottggatcc acaggaaagt cttccctggg aacagaggag 550
 cagagacott tataagactc tctacggat gtgaatcaag agaacgtccc 600
 cagctttggc atctcaagt atccccgag agcagaatag gtactccact 650
 tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700
 cagggtgcga cgctcctgtt accctttctc ttccctgttc ttgtaacatt 750
 cttgtgcttt gactccttct ccatcttttc tacctgaccc tgggtgtgaa 800
 actgcatagt gaatatcccc aacccaatg ggcattgact gtagaatacc 850
 ctagagtcc tgtagtgctc tacattaaaa atataatgct tctctctatt 900
 cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaaa aaaaaaaaaa 950
 aaaaaaaaaa aaaaaaaaaa aa 972

<210> 359
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 359
 Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu
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 20 25 30
 Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln
 35 40 45
 Leu Leu Gln Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu
 50 55 60
 Leu Lys Ala Leu Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr
 65 70 75
 Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met
 80 85 90
 Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu
 95 100 105
 Pro Ser Val Arg Val Pro Arg Pro Leu His Pro Asn Gln Leu Gly
 110 115 120

ggcdaactatg gggctctgggc tgccctctgt cctcctcttg accctccttg 100
gcagctcaca tggaacaggc cgggtatga ctttgcaact gaagctgaag 150
gagtcttttc tgacaaatcc ctccatagag tccagcttcc tggaattgct 200
tgaaaagctc tgccctctcc tccatctccc ttcaggggacc agcgtcacc 250
tccaccatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300
ttgaagcctg tgtccttctt ggcccgggct tttgggcccgg ggatgcagga 350
ggcaggcccc gacctgtct ttcagcaggc cccaccctc ctgagtggca 400
ataataaaaa ttcggtatgc tg 422

<210> 363
<211> 78
<212> PRT
<213> Homo sapiens

<400> 363
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Thr Leu Leu Gly 15
1 5 10
Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu 30
20 25
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu 45
35 40
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly 60
50 55
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val 75
65 70
Cys Asn Thr

<210> 364
<211> 826
<212> DNA
<213> Homo sapiens

<400> 364
aattgtatct gtgtaatgtt aaaacaaacg aaataaaata gaaggaaaaa 50
ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100
acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150
ttctgatgtg gggttcctcc actgtgttct gtgtgtatt aatatttacc 200
attgcagaag ctccattcag tgttgaaaaa gaatgcttag tggatctgtg 250
cctcttacgc atatgttaca aattatctgg agttcctaata caatgcagag 300
ttccctccct ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350
aaaaggcatg tatttaaata tgtatgatto toaaccatct ttagtggga 400
aaggctcttg aaagcaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttaccttttc acttagtagg atgtgttggt acgctagtaa 500
 aatagaaacc tgtgttttatt ctcagggtatt ttagaacaa cagccatcat 550
 tttattttat gtgtgtgttgc ttggctgtat tcataaatta tatattttgg 600
 gctatcaaat attacttcat tcaatataaa taacaatagt agaagttggt 650
 tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700
 ttgttgtaat agcctttgaa atttacagta ctgtctctct actatottca 750
 gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800
 accagaataa aagttcatat ctaccc 826

<210> 365
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 365
 Met Ile Gly Tyr Tyr Leu Ile Leu Phe Leu Met Trp Gly Ser Ser 15
 1 5 10
 Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser 30
 20 25
 Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg 45
 35 40
 Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro 60
 50 55
 Leu Pro Ser Asp Cys Ser Lys 65
 60

<210> 366
 <211> 2475
 <212> DNA
 <213> Homo sapiens

<400> 366
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 tgagacatcc ttgagaagag ccacagcata agagactgcc ctgcttggtg 100
 ttttcgagga tgatgggtggc ccttcgagga gcttctgcat tgctggttct 150
 gttccttgca gcttttctgc ccccgcgca gtgtaccacg gaccacgca 200
 tgggtgcatta catctaccag cgctttogag tcttgagca agggctggaa 250
 aaatgtaccc aagcaacgag ggcatacatt caagaattcc aagagtctc 300
 aaaaaatata tctgtcatgc tgggaagatg tcagacotac acaagtgagt 350
 acaagagtgc agtgggtaac ttggcactga gagttgaacg tgcccaacg 400
 gagattgact acatacaata ccttcgagag gctgacgagt gcactgtatc 450
 agaggacaag acactggcag aaatgttgct ccaagaagct gaagaagaga 500

aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550
 ataaagtctt tgaataatgt gaagaagatg atggacacac atggctcttg 600
 gatgaaagat gctgtctata actctccaaa ggtgtactta ttaattggat 650
 ccagaaccaa cactgttttg gaatttgcaa acatacgggc attcatggag 700
 gataacacca agccagctcc cgggaagcaa atcctaacac ttctctggca 750
 gggaacaggc caagtgatct acaaagggtt tctatttttt cataaccaag 800
 caacttctaa tgagataatc aatatatacc tgcagaagag gactgtggaa 850
 gatcgaatgc tgcctccagg aggggtaggc cgagcattgg ttaccagca 900
 ctccccctca acttacattg acctggctgt ggatgagcat gggctctggg 950
 ccatccactc tgggccaggc acccatagcc atttggttct cacaagatt 1000
 gagccgggca cactgggagt ggagcattca tgggataccc catgcagaag 1050
 ccaggatgct gaagccctcat tcctcttggt tggggttctc tatgtggtct 1100
 acagtactgg gggccagggc cctcatcgca tcacctgcat ctatgatcca 1150
 ctgggcacta tcagtgagga ggacttgccc aacttgttct tccccaaag 1200
 accaagaagt cactccatga tccattacaa cccagagat aagcagctct 1250
 atgcctggaa tgaaggaaac cagatcattt acaaactcca gacaaagaga 1300
 aagctgcctc tgaagtaatg cattacagct gtgagaaga gcaactgtgc 1350
 tttggcagct gttctacagg acagtgaggc tatagccctc tcacaataa 1400
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 ctccctggc ctttctgtaa gctcttccct ctttttcaaa tgtctattga 1750
 tattctccca ttttactgc ccaactaaaa tactattaat atttctttct 1800
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 tgggattaca ggcatgtgcc accacacctg gcttaaaata ctatttctta 1950
 ttgaggttta acctctattt cccctagccc tgctcttcca ctaagcttgg 2000
 tagatgtaat aataaagtga aatatataac atttgaatat cgctttccag 2050
 gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaca 2100

tgcacaagtc ttacagctg tcattctaga gtttaggtga gtaacacaat 2150
 tacaagtgaa aagatacagc tagaaaatac tacaatcccc atagtttttc 2200
 cattgcccaa ggaagcatca aatacgatatg tttgttcacc tactcttata 2250
 gtcaatgcgt tcatcgtttc agcctaaaaa taatagtcgtg tcccttttagc 2300
 cagtttttcat gtctgcacaa gacctttcaa taggcctttc aaatgataat 2350
 tcctccagaa aaccagtcta aggggtgagga ccccaactct agcctcctct 2400
 tgtcttgctg tcctctgttt ctctctttct gctttaaatt caataaaagt 2450
 gacactgagc aaaaaaaaaa aaaaa 2475

<210> 367
 <211> 402
 <212> PRT
 <213> Homo sapiens

<400> 367
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 1 5 10 15
 Leu Ala Ala Phe Leu Pro Pro Pro Gln Cys Thr Gln Asp Pro Ala
 20 25 30
 Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly
 35 40 45
 Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe
 50 55 60
 Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln
 65 70 75
 Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu
 80 85 90
 Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu
 95 100 105
 Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala
 110 115 120
 Glu Met Leu Leu Gln Glu Ala Glu Glu Glu Lys Lys Ile Arg Thr
 125 130 135
 Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser
 140 145 150
 Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met
 155 160 165
 Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly
 170 175 180
 Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe
 185 190 195
 Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr
 200 205 210

Leu Ser Trp Gln Gly Thr Gly Gln Val Ile Tyr Lys Gly Phe Leu
 215 220
 Phe Phe His Asn Gln Ala Thr Ser Asn Glu Ile Ile Lys Tyr Asn
 230 235 240
 Leu Gln Lys Arg Thr Val Glu Asp Arg Met Leu Leu Pro Gly Gly
 245 250 255
 Val Gly Arg Ala Leu Val Tyr Gln His Ser Pro Ser Thr Tyr Ile
 260 265 270
 Asp Leu Ala Val Asp Glu His Gly Leu Trp Ala Ile His Ser Gly
 275 280 285
 Pro Gly Thr His Ser His Leu Val Leu Thr Lys Ile Glu Pro Gly
 290 295 300
 Thr Leu Gly Val Glu His Ser Trp Asp Thr Pro Cys Arg Ser Gln
 305 310 315
 Asp Ala Glu Ala Ser Phe Leu Leu Cys Gly Val Leu Tyr Val Val
 320 325 330
 Tyr Ser Thr Gly Gly Gln Gly Pro His Arg Ile Thr Cys Ile Tyr
 335 340 345
 Asp Pro Leu Gly Thr Ile Ser Glu Glu Asp Leu Pro Asn Leu Phe
 350 355 360
 Phe Pro Lys Arg Pro Arg Ser His Ser Met Ile His Tyr Asn Pro
 365 370 375
 Arg Asp Lys Gln Leu Tyr Ala Trp Asn Glu Gly Asn Gln Ile Ile
 380 385 390
 Tyr Lys Leu Gln Thr Lys Arg Lys Leu Pro Leu Lys
 395 400

<210> 368

<211> 2281

<212> DNA

<213> Homo sapiens

<400> 368

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 ggaggagagg agcgcgcggc ccgcctgccca aaaagcaaat ggatttcac 200
 ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggtattcg 250
 aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300
 tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369

<211> 447

<212> PRT

<213> Homo sapiens

<400> 369

Met	Glu	Leu	Ser	Gln	Met	Ser	Glu	Leu	Met	Gly	Leu	Ser	Val	Leu
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Leu	Gly	Leu	Leu	Ala	Leu	Met	Ala	Thr	Ala	Ala	Val	Ala	Arg	Gly
			20						25					30
Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln
			35						40					45
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys
			50						55					60
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His
			65						70					75
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser
			80						85					90
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu
			95						100					105
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys
			110						115					120
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu
			125						130					135
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala
			140						145					150
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys
			155						160					165
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro
			170						175					180
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly
			185						190					195
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr
			200						205					210
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile
			215						220					225
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys
			230						235					240

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 ggtggggaca agggacaggg agcagggcag gggctgaaaag gggcactgat 1350
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 caccaactga aaaaa 1415

<210> 371
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 371
 Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr
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 Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val
 20 25 30
 Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg
 35 40 45
 Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys
 50 55 60
 His Pro Gly Ser His Lys Val Pro Phe Arg Lys Arg Lys His
 65 70 75

His	Thr	Cys	Pro	Cys	Leu	Pro	Asn	Leu	Leu	Cys	Ser	Arg	Phe	Pro
				80					85					90
Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp	Leu	Lys	Asn	Ile	Asn	Phe
				95					100					105

<210> 372
 <211> 1281
 <212> DNA
 <213> Homo sapiens

<400> 372
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 gaaatgtctt tctctcagga cccaagtctt ttcacattgg ggatgtggtc 100
 cattgggtgca ggagccctgg gggctgctgc cttggcattg ctgcttgcca 150
 acacagacgt gtttctgtcc aagccccaga aagcgccctt ggagtacctg 200
 gaggatatag acctgaaaaa actggagaag gaaccaagga ctttcaaagc 250
 aaaggagcta tgggaaaaaa atggagctgt gattatggcc gtgcggaggc 300
 caggctgttt cctctgtcga gaggaagctg cggatctgtc ctccctgaaa 350
 agcatgttgg accagctggg cgctccccctc tatgcagtgg taaaggagca 400
 catcaggact gaagtgaagg atttccagcc ttatttcaaa ggagaaatct 450
 tcctggatga aaagaaaaag ttctatggtc cacaaggcgg gaagatgatg 500
 tttatgggat ttatccgtct gggagtgtgg tacaacttct tccgagcctg 550
 gaacggaggc ttctctggaa acctggaagg agaaggcttc atccttgagg 600
 gagttttctg ggtgggatca ggaaagcagg gcattcttct tgagcaccga 650
 gaaaaagaat ttggagacaa agtaaaccta ctttctgttc tggaaagtgc 700
 taagatgatc aaaccacaga ctttggcctc agagaaaaaa tgattgtgtg 750
 aaactgcccc gctcagggat aaccagggac attcacctgt gttcatggga 800
 tgtattgttt ccaactcgtg cctaaggag tgagaaaccc atttatactc 850
 tactctcagt atggattatt aatgtatttt aatattctgt ttaggccacc 900
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 gaggattatt aagctaaaaa ctgggaaata ggaggtctaa aattgactgc 1000
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 aagggtgagca agtcacttga ggtcgggagt tcgagaccag cctgagcaac 1100
 atggcgaaac ccogtctcta ctaaaaatac aaaaatcacc cgggtgtggt 1150
 ggagggcacc tgtagtccca gctacccggg aggctgaggc aggagaatca 1200
 cttgaacctg ggaggtggag gttgcggtga gctgagatca caccactgta 1250
 ttccagcctg ggtgactgag actctaacta a 1281

<210> 373
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 373
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp
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 Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu
 20 25 30
 Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
 35 40 45
 Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu
 50 55 60
 Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
 65 70 75
 Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu
 80 85 90
 Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
 95 100 105
 Gly Val Pro Leu Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu
 110 115 120
 Val Lys Asp Phe Gln Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp
 125 130 135
 Glu Lys Lys Lys Phe Tyr Gly Pro Gln Arg Arg Lys Met Met Phe
 140 145 150
 Met Gly Phe Ile Arg Leu Gly Val Trp Tyr Asn Phe Phe Arg Ala
 155 160 165
 Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly Glu Gly Phe Ile
 170 175 180
 Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln Gly Ile Leu
 185 190 195
 Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn Leu Leu
 200 205 210
 Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu Ala
 215 220 225
 Ser Glu Lys Lys

<210> 374
 <211> 744
 <212> DNA
 <213> Homo sapiens

<400> 374
 acggaccgag gggtcgaggg agggacacgg accaggaacc tgagctaggt 50
 caaagacgcc cgggccaggt gccccgtcgc aggtgcccct ggccggagat 100

gcggtaggag gggcgagcgc gagaagcccc ttctctggcg ctgccaaacc 150
gccacccagc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg 200
cctgcgcttc ctgctggccc gctggggccg agcctggggg caaatacaga 250
ccacttctgc aaatgagaat agcactgttt tgccttcato caccagctcc 300
agctccgatg gcaacctgcg tccggaagcc atcactgcta tcactgtgtg 350
cttctocctc ttggctgctt tgctcctggc tgtggggctg gcaactgttg 400
tgcggaagct tcgggagaag cggcagacgg agggcaccta cgggccaggt 450
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caaggagacg gtgcagggct gctgcccatt ctagggtccc tctcctgcat 550
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gggcagtcag atocaccagc tgcttaatag cagggaagaa ggtacttcaa 650
agactctgcc cctgaggcca agagaggatg gggctattca cttttatata 700
tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa 744

<210> 375

<211> 123

<212> PRT

<213> Homo sapiens

<400> 375

Met	Ala	Asn	Pro	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Leu	Gly	Leu	Pro	1	5	10	15
Phe	Leu	Leu	Ala	Arg	Trp	Gly	Arg	Ala	Trp	Gly	Gln	Ile	Gln	Thr	20	25	30	
Thr	Ser	Ala	Asn	Glu	Asn	Ser	Thr	Val	Leu	Pro	Ser	Ser	Thr	Ser	35	40	45	
Ser	Ser	Ser	Asp	Gly	Asn	Leu	Arg	Pro	Glu	Ala	Ile	Thr	Ala	Ile	50	55	60	
Ile	Val	Val	Phe	Ser	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Val	Gly		65	70	75	
Leu	Ala	Leu	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Arg	Gln	Thr	Glu	80	85	90	
Gly	Thr	Tyr	Arg	Pro	Ser	Ser	Glu	Glu	Gln	Phe	Ser	His	Ala	Ala	95	100	105	
Glu	Ala	Arg	Ala	Pro	Gln	Asp	Ser	Lys	Glu	Thr	Val	Gln	Gly	Cys	110	115	120	
Leu	Pro	Ile																

<210> 376

<211> 713

<212> DNA

<213> Homo sapiens

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 ccagaagatg aaaaaataat tgaacaata gaggatattg tgactacagc 200
 ttctacgtac ctgtttgaag ccacagaaaa aagatttttt tcaaaaaatg 250
 tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg 300
 ccaaaacatg aaaaccataa acatgctgat gttatagttg caccacctac 350
 actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag 400
 agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa 450
 caaaatgaat atggaccacc aggcaaaactg tttgtccatg agtgggctca 500
 cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc 550
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 ggtagaaata gagtttataa gtgtcaagga ggcagctgtc ttagtagagc 650
 atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct 700
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 aatccaaata aaaagcagtg atgaaagaaa cacactcatg gcaggattac 1150
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3250

aaaaaaaaaaaa 3265

<210> 379

<211> 919

<212> PRT

<213> Homo sapiens

<400> 379

Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu
1 5 10 15
Leu His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly
20 25 30
Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp
35 40 45
Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser
50 55 60
Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn
65 70 75
Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr
80 85 90
Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val
95 100 105
Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln
110 115 120
Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro
125 130 135
Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly
140 145 150
Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe
155 160 165
Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys
170 175 180
Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn
185 190 195
Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys
200 205 210
Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe
215 220 225
Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
230 235 240
Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His
245 250 255
Asn Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg
260 265 270
Ser Thr Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr

275	280	285
Ile Pro Met Val Thr Pro Pro Pro Pro	Pro Val Phe Ser Leu Leu	
290	295	300
Lys Ile Ser Gln Arg Ile Val Cys Leu	Val Leu Asp Lys Ser Gly	
305	310	315
Ser Met Gly Gly Lys Asp Arg Leu Asn	Arg Met Asn Gln Ala Ala	
320	325	330
Lys His Phe Leu Leu Gln Thr Val Glu	Asn Gly Ser Trp Val Gly	
335	340	345
Met Val His Phe Asp Ser Thr Ala Thr	Ile Val Asn Lys Leu Ile	
350	355	360
Gln Ile Lys Ser Ser Asp Glu Arg Asn	Thr Leu Met Ala Gly Leu	
365	370	375
Pro Thr Tyr Pro Leu Gly Gly Thr Ser	Ile Cys Ser Gly Ile Lys	
380	385	390
Tyr Ala Phe Gln Val Ile Gly Glu Leu	His Ser Gln Leu Asp Gly	
395	400	405
Ser Glu Val Leu Leu Leu Thr Asp Gly	Glu Asp Asn Thr Ala Ser	
410	415	420
Ser Cys Ile Asp Glu Val Lys Gln Ser	Gly Ala Ile Val His Phe	
425	430	435
Ile Ala Leu Gly Arg Ala Ala Asp Glu	Ala Val Ile Glu Met Ser	
440	445	450
Lys Ile Thr Gly Gly Ser His Phe Tyr	Val Ser Asp Glu Ala Gln	
455	460	465
Asn Asn Gly Leu Ile Asp Ala Phe Gly	Ala Leu Thr Ser Gly Asn	
470	475	480
Thr Asp Leu Ser Gln Lys Ser Leu Gln	Leu Glu Ser Lys Gly Leu	
485	490	495
Thr Leu Asn Ser Asn Ala Trp Met Asn	Asp Thr Val Ile Ile Asn	
500	505	510
Ser Thr Val Gly Lys Asp Thr Phe Phe	Leu Ile Thr Trp Asn Ser	
515	520	525
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Glu Asn Phe Thr Val Asp Ala Thr Ser	Lys Met Ala Tyr Leu Ser	
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Ile Pro Gly Thr Ala Lys Val Gly Thr	Trp Ala Tyr Asn Leu Gln	
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Ala Lys Ala Asn Pro Glu Thr Leu Thr	Ile Thr Val Thr Ser Arg	
575	580	585
Ala Ala Asn Ser Ser Val Pro Pro Ile	Thr Val Asn Ala Lys Met	

590	595	600
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605	610	615
Glu Ile Leu Gln	Gly Tyr Val Pro Val	Leu Gly Ala Asn Val Thr
620	625	630
Ala Phe Ile Glu	Ser Gln Asn Gly His	Thr Glu Val Leu Glu
635	640	645
Leu Asp Asn Gly	Ala Gly Ala Asp Ser	Phe Lys Asn Asp Gly
650	655	660
Tyr Ser Arg Tyr	Phe Thr Ala Tyr Thr	Glu Asn Gly Arg Tyr
665	670	675
Leu Lys Val Arg	Ala His Gly Gly Ala	Asn Thr Ala Arg Leu
680	685	690
Leu Arg Pro Pro	Leu Asn Arg Ala Ala	Tyr Ile Pro Gly Trp
695	700	705
Val Asn Gly Glu	Ile Glu Ala Asn Pro	Pro Arg Pro Glu Ile
710	715	720
Glu Asp Thr Gln	Thr Thr Leu Glu Asp	Phe Ser Arg Thr Ala
725	730	735
Gly Gly Ala Phe	Val Val Ser Gln Val	Pro Ser Leu Pro Leu
740	745	750
Asp Gln Tyr Pro	Pro Ser Gln Ile Thr	Asp Leu Asp Ala Thr
755	760	765
His Glu Asp Lys	Ile Ile Leu Thr Trp	Thr Ala Pro Gly Asp
770	775	780
Phe Asp Val Gly	Lys Val Gln Arg Tyr	Ile Ile Arg Ile Ser
785	790	795
Ser Ile Leu Asp	Leu Arg Asp Ser Phe	Asp Asp Ala Leu Gln
800	805	810
Asn Thr Thr Asp	Leu Ser Pro Lys Glu	Ala Asn Ser Lys Glu
815	820	825
Phe Ala Phe Lys	Pro Glu Asn Ile Ser	Glu Glu Asn Ala Thr
830	835	840
Ile Phe Ile Ala	Ile Lys Ser Ile Asp	Lys Ser Asn Leu Thr
845	850	855
Lys Val Ser Asn	Ile Ala Gln Val Thr	Leu Phe Ile Pro Gln
860	865	870
Asn Pro Asp Asp	Ile Asp Pro Thr Pro	Thr Pro Thr Pro Thr
875	880	885
Thr Pro Asp Lys	Ser His Asn Ser Gly	Val Asn Ile Ser Thr
890	895	900
Val Leu Ser Val	Ile Gly Ser Val Val	Ile Val Asn Phe Ile
		Leu

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<210> 380
<211> 3877
<212> DNA
<213> Homo sapiens
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gaccacagag agcaatgatg tagccacctc ctaaccttcc cttcttgaac 200
ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg 250
gctccttcgg cttaaacttg ggttgaggga gagaaccttt gtgggggtgc 300
gttctcttag cagtgtctag aagtgacttg cctgagggtg gaccagaaga 350
aaggaaaagt cccctcttgc tgttggtctg acatcaggaa ggctgtgatg 400
ggaatgaagg tgaaaaactg gagatttcac ttcagtcatt gottctgcct 450
ccaagatcat cttttaaaag tagagaagct gctctgtgtg gtggttaact 500
ccaagaggca gaactcgttc tagaaggaaa tggatgcaag cagctccggg 550
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caatcacctt ccttacacgg cctctgattt catagaaggg atctaccgaa 1300

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09929312011

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Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly	
				95					100					105	
Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu	
				110					115					120	
Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala	
				125					130					135	
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser	
				140					145					150	
Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg	
				155					160					165	
His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu	
				170					175					180	
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala	
				185					190					195	
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile	
				200					205					210	
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu	
				215					220					225	
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile	
				230					235					240	
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys	
				245					250					255	
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala	
				260					265					270	
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu	
				275					280					285	
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr	
				290					295					300	
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn	
				305					310					315	
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu	
				320					325					330	
Asn	Gly	Glu	Phe	Ser	Arg	Gly	Lys	Gly	Leu	Asp	Val	Gly	Ala	Arg	
				335					340					345	
Phe	Trp	Lys	Gly	Ser	Asn	Val	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	
				350					355					360	
Ile	Tyr	Phe	Thr	Ser	Glu	Phe	Leu	Asn	Thr	Cys	Arg	Leu	Asn	Thr	
				365					370					375	
Gln	Pro	Gly	Lys	Lys	Val	Phe	Tyr	Pro	Val	Leu	Phe	Ser	Gln	Tyr	
				380					385					390	
Asn	Pro	Gly	Ile	Ile	Tyr	Gly	His	His	Asp	Ala	Val	Pro	Pro	Leu	
				395					400					405	

Glu Gln Gln Leu Val Ile Lys Lys Glu Thr Gly Phe Trp Arg Asp
410 415 420

Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Ile Asn
425 430 435

Ile Gly Gly Phe Asp Leu Asp Ile Lys Gly Trp Gly Gly Glu Asp
440 445 450

Val His Leu Tyr Arg Lys Tyr Leu His Ser Asn Leu Ile Val Val
455 460 465

Arg Thr Pro Val Arg Gly Leu Phe His Leu Trp His Glu Lys Arg
470 475 480

Cys Met Asp Glu Leu Thr Pro Glu Gln Tyr Lys Met Cys Met Gln
485 490 495

Ser Lys Ala Met Asn Glu Ala Ser His Gly Gln Leu Gly Met Leu
500 505 510

Val Phe Arg His Glu Ile Glu Ala His Leu Arg Lys Gln Lys Gln
515 520 525

Lys Thr Ser Ser Lys Lys Thr
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<210> 382
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 383
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
gcgaagggtga gcctctatct cgtgcc 26

<210> 384
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagcctacac gtattgagg 19

<210> 385
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

cagtcagttac aatcctggca taatatacgg ccacatgat gcagtgccc 48

<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

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ctcttcaaa cgatggtagc ttttccatg agaaaagtgc ccaacagaga 200
agcaacagaa atttcccatg tctactttg caatgtaacc cagagggtat 250
cattctggtt tgtggttaca gaccttcaa aaaatcacac ccttctgct 300
gttgagggtc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350
cttctttcta aatgaccaa ctotggaatt tttaaaaatc ccttccacac 400
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gttgattata ttttttctga atatcagccc ctaaataggac aattctattt 1250

gttgaccatt totacaattt gtaaaagtcc aatctgtgct aacttaataa 1300
 agtaataatc atctcttttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1346

<210> 387
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 387
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 20 25 30
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 35 40 45
 Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys
 50 55 60
 Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys
 65 70 75
 Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro
 80 85 90
 Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile
 95 100 105
 Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
 110 115 120
 Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
 125 130 135
 Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile
 140 145 150
 Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly
 155 160 165
 Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp
 170 175 180
 Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly
 185 190 195
 Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met
 200 205 210
 Pro Ser

<210> 388
 <211> 1371
 <212> DNA
 <213> Homo sapiens

<400> 388
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 gtgacctgga attttcgtcc tctagacggg ggacctgagc agtttgtatt 350
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 aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggt cctgtgttat 750
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 tctccttaac tatgagacac atcttggttt actgaatttc tttcaattat 1350
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<210> 389
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 389
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Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
				35					40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
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Leu	Glu	Asp	Thr	Asp											
				215											

<210> 390

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

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<210> 391

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

acaggcagag ccaatggcca gaggc 24

<210> 392
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcattg 45

<210> 393
<211> 471
<212> DNA
<213> Homo sapiens

<400> 393
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gatgatgaag cccctgatgc tgaaccact gctgctgcaa ccactgcgac 200
cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250
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ccctttatc tctaatacgt ttattttctt tcaataaaaa aataactatg 450
agcaacataa aaaaaaaaaa a 471

<210> 394
<211> 90
<212> PRT
<213> Homo sapiens

<400> 394
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe
1 5 10 15
Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
20 25 30
Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
35 40 45
Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
50 55 60
Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
65 70 75
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
80 85 90

<210> 395
<211> 25

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 395
 gtcctctgat cttcatgtca ccacc 25

 <210> 396
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 396
 cagggacaca ctctaccatt cgggag 26

 <210> 397
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 397
 ccatctttct ggtctctgcc cagaatccga caacagctgc tc 42

 <210> 398
 <211> 907
 <212> DNA
 <213> Homo sapiens

 <400> 398
 ggactctgaa ggtcccaagc agctgctgag gccccaagg aagtggttcc 50
 aaccttgac ccctaggggt ctggatttgc tggttaaca gataacctga 100
 gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150
 gtgttcacgg tggcctgggc cctccttgcc gagagagtgt cctgggtcag 200
 ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250
 ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300
 gcaggagggg gacagttctg ttgtgcttgg ttggacagta agaggggtctt 350
 ggccagtcca ggggtggggg cggcaaaact cataaagaac cagagggtct 400
 gggccccggc cacagagtca tctgccagc tcctctgctg ctggccagtg 450
 ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500
 gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550
 ttccaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600
 agcaattaaa actgagaaat gggccgggca cggtggctca cgcctgtaat 650

tagaagtoca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450
 gaggtctctaa aggctcacgc tgacaagcag agccacatcc tatgggccct 500
 cacaggccac gtgcagcggc agaggcggga gatgggtgca cagcagcatc 550
 ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600
 atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650
 cgcacctga ggcacctgtg caggaggagg ctgcctgttc actgggatca 700
 gccaggcgcc cgggcccccac ttctgagcac agagcagaga cagacgcagg 750
 cggggacaaa ggcagaggat gtagcccatc tggggagggg tggaggaagg 800
 acatgtaccc ttctatgcct acacaccctt cattaaagca gactcgtggc 850
 atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 401
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val 15
 1 5 10
 Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala 30
 20 25
 Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu 45
 35 40
 Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu 60
 50 55
 Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu 75
 65 70
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu 90
 80 85
 Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu 105
 95 100
 Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala 120
 110 115
 Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val 135
 125 130
 Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu 150
 140 145
 Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala 165
 155 160
 Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln 180
 170 175
 Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala

Leu Pro Ala

<210> 402
 <211> 1915
 <212> DNA
 <213> Homo sapiens

<400> 402
 ggcaacatgg ctcagcaggc ttgccccaga gccatggcaa agaattggact 50
 tgtaatttgc atcctggtga tcaccttact cctggaccag accaccagcc 100
 acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150
 aaggatggag atctgaagac tcaaatgaa aagctctgga cagaagtcga 200
 tgccctgaag gaaattcaag cctgcagac agtctgtctc cgaggcacta 250
 aagttcaca gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300
 gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350
 gaactccgac gaaatcaacg cctccaaga ctatggtaaa aggagcctgc 400
 cagggtgcaa tgacttttgg ctgggcatca atgacatggt cagcgaaggc 450
 aagtttgttg acgtcaacgg aatcgtctatc tcttctctca actgggacgc 500
 tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550
 cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatgc 600
 atatgogagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650
 agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700
 aatcataatt ttacttatt aaaaaattgc aacacaagat caatgtccat 750
 agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800
 tgccttctct ggggtatagg ggtacagaaa tattgatcca tgtgcacgca 850
 gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900
 tcacttgtac aaaccaggtt tgttttcaaa aaatcacagt agcaatgcaa 950
 ctcatcactc tagaaaagca agcttaggct acctgaaaga ttttcccttg 1000
 gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050
 aggtgctata taatccaaaa acttttcagc ctgttgctca tctgtccca 1100
 tgctggcaat aataccttgt cagcccatta ccttattttt gaattgctcc 1150
 atctcctggt gggacttgta tcttgtctgc catatcagaa cacaaacccc 1200
 tgaagaggtt ctgatttgat tttttttttt tcttcatgcc tacocctttt 1250
 ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatattg 1300

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400
 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450
 aaaccccgcc gcggggagga cgtccatcc ccttcccccg gccctctca 500
 ataacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550
 aaaaaaaaaa aaaaaaaaaa 570

<210> 408
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys
 1 5 10 15
 Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala
 20 25 30
 Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly
 35 40 45
 Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu
 50 55 60
 Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser
 65 70 75
 Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val
 80 85 90
 Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly
 95 100

<210> 409
 <211> 2089
 <212> DNA
 <213> Homo sapiens

<400> 409
 tgaaggactt ttccaggacc caaggccaca cactggaagt cttgcagctg 50
 aaggaggcca ctccctggcc tcgcagccg atcacatgaa ggtggtgcc 100
 agtctctgc tctcgtctc cctggcacag gtgtggtctg tacccggtt 150
 gggcccccagt cctcagtcgc cagagacccc agccctcag aaccagacca 200
 gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250
 agcgaggaga aggccgttga ggaagagaaa gcctggctga tggccagcag 300
 gcagcagctt gccaaaggaga cttcaaaact cggtattcagc ctgctgcgaa 350
 agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400
 tccttgccca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450
 ccagatcaag agagggtctc acttgaggc cctgaagccc accaagccc 500

<210> 410
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 410

Met	Lys	Val	Val	Pro	Ser	Leu	Leu	Leu	Ser	Val	Leu	Leu	Ala	Gln
1				5					10					15
Val	Trp	Leu	Val	Pro	Gly	Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu
				20					25					30
Thr	Pro	Ala	Pro	Gln	Asn	Gln	Thr	Ser	Arg	Val	Val	Gln	Ala	Pro
				35					40					45
Arg	Glu	Glu	Glu	Glu	Asp	Glu	Gln	Glu	Ala	Ser	Glu	Glu	Lys	Ala
				50					55					60
Gly	Glu	Glu	Glu	Lys	Ala	Trp	Leu	Met	Ala	Ser	Arg	Gln	Gln	Leu
				65					70					75
Ala	Lys	Glu	Thr	Ser	Asn	Phe	Gly	Phe	Ser	Leu	Leu	Arg	Lys	Ile
				80					85					90
Ser	Met	Arg	His	Asp	Gly	Asn	Met	Val	Phe	Ser	Pro	Phe	Gly	Met
				95					100					105
Ser	Leu	Ala	Met	Thr	Gly	Leu	Met	Leu	Gly	Ala	Thr	Gly	Pro	Thr
				110					115					120
Glu	Thr	Gln	Ile	Lys	Arg	Gly	Leu	His	Leu	Gln	Ala	Leu	Lys	Pro
				125					130					135
Thr	Lys	Pro	Gly	Leu	Leu	Pro	Ser	Leu	Phe	Lys	Gly	Leu	Arg	Glu
				140					145					150
Thr	Leu	Ser	Arg	Asn	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Phe
				155					160					165
Ala	Phe	Ile	His	Lys	Asp	Phe	Asp	Val	Lys	Glu	Thr	Phe	Phe	Asn
				170					175					180
Leu	Ser	Lys	Arg	Tyr	Phe	Asp	Thr	Glu	Cys	Val	Pro	Met	Asn	Phe
				185					190					195
Arg	Asn	Ala	Ser	Gln	Ala	Lys	Arg	Leu	Met	Asn	His	Tyr	Ile	Asn
				200					205					210
Lys	Glu	Thr	Arg	Gly	Lys	Ile	Pro	Lys	Leu	Phe	Asp	Glu	Ile	Asn
				215					220					225
Pro	Glu	Thr	Lys	Leu	Ile	Leu	Val	Asp	Tyr	Ile	Leu	Phe	Lys	Gly
				230					235					240
Lys	Trp	Leu	Thr	Pro	Phe	Asp	Pro	Val	Phe	Thr	Glu	Val	Asp	Thr
				245					250					255
Phe	His	Leu	Asp	Lys	Tyr	Lys	Thr	Ile	Lys	Val	Pro	Met	Met	Tyr
				260					265					270
Gly	Ala	Gly	Lys	Phe	Ala	Ser	Thr	Phe	Asp	Lys	Asn	Phe	Arg	Cys
				275					280					285

His Val Leu Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val
 290 295 300
 Val Leu Met Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr
 305 310 315
 Leu Thr Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr
 320 325 330
 Arg Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
 335 340 345
 Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg Ile
 350 355 360
 Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg
 365 370 375
 Asn Leu Gln Val Ser Arg Val Leu Arg Arg Thr Val Ile Glu Val
 380 385 390
 Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile
 395 400 405
 Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
 410 415 420
 His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe Leu
 425 430 435
 Gly Arg Val Val Asn Pro Thr Leu Leu
 440

<210> 411

<211> 636

<212> DNA

<213> Homo sapiens

<400> 411

ctgggatcag ccaactgcagc tccctgagca ctctctacag agacgcggac 50
 cccagacatg aggaggctcc tcttggtcac cagcctggtg gttgtgctgc 100
 tgtgggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150
 gtcaaacact ggcctcaga gcaggaccca gagaaggcct ggggcgcccg 200
 tgtgtgtgag cctccggaga aggacgacca gctgggtggtg ctgttccctg 250
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300
 aggggcccc tcttccagg caccaaggcc tggatggaga ccgaggacac 350
 cctgggcccgt gtctctgagtc ccgagcccga ccatgacagc ctgtaccacc 400
 ctccgcctga ggaggaccag ggcgaggaga ggcgccggtt gtgggtgatg 450
 ccaaatacacc aggtgctcct gggaccggag gaagaccaag accacatcta 500
 ccacccccag tagggctcca ggggccatca ctgccccgcg cctgtcccaa 550
 ggcccaggct gttgggactg ggaccctccc taccctgccc cagctagaca 600

aataaacccc agcaggCaaa aaaaaaaaaa aaaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu
1 5 10
Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met
20 25 30
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp
35 40 45
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val
50 55 60
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu
65 70 75
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys
80 85 90
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro
95 100 105
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
110 115 120
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln
125 130 135
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro
140 145 150
Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac 300
cagaccttct gtgacatgac ctctgggggt ggcggctgga cctgtgtggc 350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacgggt ggcgatcgct 400

ggtccagtcg gcagggcagc aaagcagact acccagaggg ggacggcaac 450
 tgggccaact acaacacctt tggatctgca gaggcgccca cgagcgatga 500
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550
 ggacagtgcc caataagtc cccatgcagc actggagaaa cagctccctg 600
 ctgaggtacc gcacggacac tggcttctc cagacactgg gacataatct 650
 gtttggcatc taccagaaat atccagtga atattggaga ggaaagtgtt 700
 ggactgacaa cggcccggtg atccctgtgg tctatgattt tggcgacgcc 750
 cagaaaacag catcttatta ctcacctat ggccagcggg aattcactgc 800
 gggattttgt cagttcaggg tatttaataa cgagagagca gccaacgcct 850
 tgtgtgctgg aatgagggtc accggtgta acactgagca tcaactgcatt 900
 ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950
 ttctggtttt gattggagtg gatatggaac tcattgttgt tacagcagca 1000
 gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050
 tgtggagggg aaccagacc tctctccca accatgagat cccaaggatg 1100
 gagaacaact taccagtag ctagaatgtt aatggcagaa gaaaaacaa 1150
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg
 1 5 10 15
 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
 20 25 30
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
 35 40 45
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
 50 55 60
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
 65 70 75
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
 80 85 90
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
 95 100 105
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
 110 115 120
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys

125	130	135
Asn Pro Gly Tyr Tyr Asp Ile Gln Ala	Lys Asp Leu Gly Ile Trp	
140	145	150
His Val Pro Asn Lys Ser Pro Met Gln	His Trp Arg Asn Ser Ser	
155	160	165
Leu Leu Arg Tyr Arg Thr Asp Thr Gly	Phe Leu Gln Thr Leu Gly	
170	175	180
His Asn Leu Phe Gly Ile Tyr Gln Lys	Tyr Pro Val Lys Tyr Gly	
185	190	195
Glu Gly Lys Cys Trp Thr Asp Asn Gly	Pro Val Ile Pro Val Val	
200	205	210
Tyr Asp Phe Gly Asp Ala Gln Lys Thr	Ala Ser Tyr Tyr Ser Pro	
215	220	225
Tyr Gly Gln Arg Glu Phe Thr Ala Gly	Phe Val Gln Phe Arg Val	
230	235	240
Phe Asn Asn Glu Arg Ala Ala Asn Ala	Leu Cys Ala Gly Met Arg	
245	250	255
Val Thr Gly Cys Asn Thr Glu His His	Cys Ile Gly Gly Gly Gly	
260	265	270
Tyr Phe Pro Glu Ala Ser Pro Gln Gln	Cys Gly Asp Phe Ser Gly	
275	280	285
Phe Asp Trp Ser Gly Tyr Gly Thr His	Val Gly Tyr Ser Ser Ser	
290	295	300
Arg Glu Ile Thr Glu Ala Ala Val Leu	Leu Phe Tyr Arg	
305	310	

<210> 415
 <211> 1281
 <212> DNA
 <213> Homo sapiens

<400> 415
 gcggagccgg cgccggctgc gcagaggagc cgctctcgcc gccgccacct 50
 cggtcgggag cccacgaggc tgccgcattc tgccctcgga acaatgggac 100
 tcggcgcgcg aggtgcttgg gccgcgctgc tctctggggac gctgcagggtg 150
 ctacgcgtgc tggggggccgc ccatgaaagc gcagccattg cgcatctgc 200
 aaacatagag aattctgggc ttccacacaa ctccagtgtc aactcaacag 250
 agactotcca acatgtgcct tctgaccata caaatgaaac ttccaacagt 300
 actgtgaaac caccaacttc agttgcctca gactccagta atacaacggt 350
 caccacatg aaacctacag cggcatctaa tacaacaaca ccagggatgg 400
 tctcaacaaa tatgacttct accaccttaa agtctacacc caaaacaaca 450
 agtgtttcac agaacacatc tcagatatca acatccacaa tgaccgtaac 500

ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550
 ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600
 gttggtggtta ttgtattaac gctgggagtt ttatctatto tttacattgg 650
 atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700
 aacatgatgc catcatttaa ggaaatccat ggaccaagga tggaatacag 750
 attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800
 tttctctttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850
 gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttgggttt 900
 tgaataaacc atctggatct tatagaccgt tcatacaatg gttttagcaa 950
 gttcatagta agacaaacaa gtctatctt ttttttttgg ctgggtggg 1000
 ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050
 agaatgcatc ctgggcatac aaataagaag tttgtcacag cactcaggat 1100
 tttgggtatc tttttagtct cacataaaga acttcagtgc ttttcagagc 1150
 tggatatatc ttaattacta atgccacaca gaaattatac aatcaaaacta 1200
 gatctgaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250
 tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416
 <211> 208
 <212> PRT
 <213> Homo sapiens

<400> 416
 Met Gly Leu Gly Ala Arg Gly Ala Trp Ala Ala Leu Leu Leu Gly
 1 5 10 15
 Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala
 20 25 30
 Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His
 35 40 45
 Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser
 50 55 60
 Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr
 65 70 75
 Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys
 80 85 90
 Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr
 95 100 105
 Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser
 110 115 120
 Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val

125	130	135
Thr His Asn Ser Ser Val Thr Ser Ala	Ala Ser Ser Val Thr Ile	
140	145	150
Thr Thr Thr Met His Ser Glu Ala Lys	Lys Gly Ser Lys Phe Asp	
155	160	165
Thr Gly Ser Phe Val Gly Gly Ile Val	Leu Thr Leu Gly Val Leu	
170	175	180
Ser Ile Leu Tyr Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg Gly	
185	190	195
Ile Arg Tyr Arg Thr Ile Asp Glu His	Asp Ala Ile Ile	
200	205	

<210> 417
 <211> 1728
 <212> DNA
 <213> Homo sapiens

<400> 417
 cagccggggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccca 50
 gccgggagcc ggctcggggg gctccgggct gtgggaccgc tggggcccca 100
 gcgatggcga cctgtgggg aggccttctt cggcttggtc ccttgctcag 150
 cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgagc ctgtcagacg 200
 ccgccaaagaa ttctgaggat gtcagatgta aatgtatctg ccctccctat 250
 aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300
 tgattgcctt catgtttgtg agcccatgcc tgtgcggggg cctgatgtag 350
 aagcatactg tctacgctgt gaatgcaa atgaagaaag aagctctgtc 400
 acaatcaagg ttaccattat aatttatctc tccattttgg gccttctact 450
 tctgtacatg gtatatctta ctctggttga gccatactg aagaggcgcc 500
 tctttggaca tgcacagttg atacagagtg atgatgat tggggatcac 550
 cagccttttg caaatgcaca cgatgtgcta gcccgctccc gcagtcgagc 600
 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650
 tccaagagca gcgaaagtct gtctttgacc ggcagttgtt cctcagctaa 700
 ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750
 agaactgact gggttttgct gggtttcatt ttaataacct gttgatttca 800
 ccaactgttg ctggaagatt caaaactgga agcaaaaaact tgcttgattt 850
 tttttctctg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900
 aaagtgcgcc aataagtctt ttccattttg tgacttttac taataaaaa 950
 aaatctgcct gtaaattatc ttgaagtctt ttacctggaa caagcactct 1000

His Ala Gln Leu Ile Gln Ser Asp Asp Ile Gly Asp His Gln
 140 145 150

Pro Phe Ala Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg
 155 160 165

Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys
 170 175 180

Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp Arg His Val
 185 190 195

Val Leu Ser

<210> 419
 <211> 681
 <212> DNA
 <213> Homo sapiens

<400> 419
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 gccttcctgt ccgcgggaa gcggcaggag ccgccgccga cacctgaagg 150
 aaaattgggc cgatttccac ctatgatgca tcatcaccag gccacctcag 200
 atggccagac tcctggggct cgtttccaga ggtctcacct tgcgaggca 250
 ttgcaaagg ccaaaggatc aggtggaggt gctggaggag gaggtattgg 300
 aagaggctct atggggcaga ttattccaat ctacggtttt gggatttttt 350
 tatatatact gtacattcta ttaaggtaa gtagaatcat cctaatacata 400
 ttacatcaat gaaaatctaa tatggcgata aaatcattg tctacattaa 450
 aactcttat agttcataaa attatttcaa atccatcacc tctttaaatc 500
 ctgctctctc ttcagaggt acttaggata gccattattt cagtttcaca 550
 taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600
 acaaggcaga actaggactt gaacatggat cttttgggtc ttaatccagt 650
 gagtataca attcaatgca ctcccctgcc a 681

<210> 420
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu
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Val Leu Ala Leu Ser Leu Leu Leu Pro Lys Ala Phe Leu Ser Arg
 20 25 30

Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly
 35 40 45

155	160	165
Thr Lys Val Glu Trp	Ile Phe Ser Gly Arg Arg Ala Lys Glu	Glu
170	175	180
Ile Val Phe Arg Tyr	Tyr His Lys Leu Arg Met Ser Val Glu Tyr	195
185	190	
Ser Gln Ser Trp Gly	His Phe Gln Asn Arg Val Asn Leu Val Gly	210
200	205	
Asp Ile Phe Arg Asn	Asp Gly Ser Ile Met Leu Gln Gly Val Arg	225
215	220	
Glu Ser Asp Gly Gly	Asn Tyr Thr Cys Ser Ile His Leu Gly Asn	240
230	235	
Leu Val Phe Lys Lys	Thr Ile Val Leu His Val Ser Pro Glu Glu	255
245	250	
Pro Arg Thr Leu Val	Thr Pro Ala Ala Leu Arg Pro Leu Val Leu	270
260	265	
Gly Gly Asn Gln Leu	Val Ile Ile Val Gly Ile Val Cys Ala Thr	285
275	280	
Ile Leu Leu Leu Pro	Val Leu Ile Leu Ile Val Lys Lys Thr Cys	300
290	295	
Gly Asn Lys Ser Ser	Val Asn Ser Thr Val Leu Val Lys Asn Thr	315
305	310	
Lys Lys Thr Asn Pro	Glu Ile Lys Glu Lys Pro Cys His Phe Glu	330
320	325	
Arg Cys Glu Gly Glu	Lys His Ile Tyr Ser Pro Ile Ile Val Arg	345
335	340	
Glu Val Ile Glu Glu	Glu Glu Pro Ser Glu Lys Ser Glu Ala Thr	360
350	355	
Tyr Met Thr Met His	Pro Val Trp Pro Ser Leu Arg Ser Asp Arg	375
365	370	
Asn Asn Ser Leu Glu	Lys Lys Ser Gly Gly Gly Met Pro Lys Thr	390
380	385	
Gln Gln Ala Phe		

<210> 423
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 423
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 ctctgagctc agttgcagta ctcggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaac cagctctcgt ctccgttggc 250
 cctgcacctt cctcctggtg gcgtgtgatg gctttgattc tgcctgatcct 300
 gtgcgtgggg atggttgtcg ggctgggtggc tctggggatt tggctgtgca 350
 tgcagcgcaa ttacctacaa gatgagaatg aaaatcgcac aggaactctg 400
 caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450
 aaagggcact ttcaaaggct ataaatgcag cccctgtgac acaaaactgga 500
 gatattatgg agatagctgc tatgggttct tcaggcacaa cttaacatgg 550
 gaagagagta agcagtactg cactgacatg aatgctactc toctgaagat 600
 tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650
 gttgggtcgg attatctcgc cagaagtoga atgaggtctg gaagtgggag 700
 gatggctcgg ttatctcaga aaatatgttt gaggtttttg aagatggaaa 750
 aggaaatatg aattgtgctt attttcataa tgggaaaatg caccctacct 800
 tctgtgagaa caaacattat ttaatgtgtg agaggaaggc tggcatgacc 850
 aaggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900
 aagggcttta ttgtacaata aaagatatgt atgaatgcat cagtagctga 950
 aaaaaaaaaa aaa 963

<210> 424

<211> 229

<212> PRT

<213> Homo sapiens

<400> 424

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Lys	Pro	Ala	Leu	Val	Ser	Val	Gly	Pro	Ala	Ser	Ser	Ser	Trp	Trp
				20					25					30
Arg	Val	Met	Ala	Leu	Ile	Leu	Leu	Ile	Leu	Cys	Val	Gly	Met	Val
				35					40					45
Val	Gly	Leu	Val	Ala	Leu	Gly	Ile	Trp	Ser	Val	Met	Gln	Arg	Asn
				50					55					60
Tyr	Leu	Gln	Asp	Glu	Asn	Glu	Asn	Arg	Thr	Gly	Thr	Leu	Gln	Gln
				65					70					75
Leu	Ala	Lys	Arg	Phe	Cys	Gln	Tyr	Val	Val	Lys	Gln	Ser	Glu	Leu
				80					85					90
Lys	Gly	Thr	Phe	Lys	Gly	His	Lys	Cys	Ser	Pro	Cys	Asp	Thr	Asn
				95					100					105
Trp	Arg	Tyr	Tyr	Gly	Asp	Ser	Cys	Tyr	Gly	Phe	Phe	Arg	His	Asn
				110					115					120
Leu	Thr	Trp	Glu	Glu	Ser	Lys	Gln	Tyr	Cys	Thr	Asp	Met	Asn	Ala

<400> 428
ccaccaatgg cagccccacc t 21

<210> 429
<211> 17
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<220>
<223> Synthetic oligonucleotide probe

<400> 429
gactgccctc cctgcca 17

<210> 430
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 430
caaaaagcct ggaagtcctc aaag 24

<210> 431
<211> 20
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<220>
<223> Synthetic oligonucleotide probe

<400> 431
cagctggact gcagtgcta 20

<210> 432
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 432
cagtgagcac agcaagtgtc ct 22

<210> 433
<211> 28
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 433
ggccacotcc ttgagtcttc agttccct 28

<210> 434
<211> 24
<212> DNA
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<220>
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<400> 434
caactactgg ctaaagctgg tgaa 24

<210> 435
<211> 27
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 435
cctttctgta taggtgatac ccaatga 27

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
tggccatccc taccagaggc aaaa 24

<210> 437
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 437
ctgaagacga cgcggtattac ta 22

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 438
ggcagaaatg ggaggcaga 19

<210> 439
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
tgctctgttg gctacggctt tagtccctag 30

<210> 440
<211> 22

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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 440
agcagcagcc atgtagaatg aa 22

<210> 441
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
aatacgaaca gtgcacgctg at 22

<210> 442
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tccagagagc caagcacggc aga 23

<210> 443
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
tctagccagc ttggtccaa ta 22

<210> 444
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
cctggctcta gcaccaactc ata 23

<210> 445
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
tcagtggccc taaggagatg ggcct 25

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<210> 446
<211> 24
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<220>
<223> Synthetic oligonucleotide probe

<400> 446
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<210> 447
<211> 22
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 447
cctgaagggc ttggagctta gt 22

<210> 448
<211> 24
<212> DNA
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<220>
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<400> 448
tctttggcca tttcccatgg ctca 24

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
cccatggcga ggaggaat 18

<210> 450
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
tgcgtacgtg tgccttcag 19

<210> 451
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 451
cagcacccca ggcagtctgt gtgt 24

<210> 452
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 452
aacgtgctac acgaccagtg tact 24

<210> 453
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
cacagcatat tcagatgact aaatcca 27

<210> 454
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ttgttttagtt ctccaccgtg tctccacaga a 31

<210> 455
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
tgtcagaatg caacctggct t 21

<210> 456
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 456
tgatgtgcct ggctcagaac 20

<210> 457
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 457
    tgcacctaga tgtccccagc accc 24

<210> 458
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 458
    aagatgcgcc aggcttctta 20

<210> 459
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 459
    ctctgtacg gtctgctcac ttat 24

<210> 460
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 460
    tggctgtcag tccagtgtgc atgg 24

<210> 461
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
    gcatagggat agataagatc ctgctttat 29

<210> 462
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 462
    caaatataag taccatcag gagagaa 27

<210> 463
<211> 37

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<212> DNA
<213> Artificial Sequence

<220>
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<400> 463
aagttgctaa atatatacat tatctgcgcc aagtcca 37

<210> 464
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 464
gtgctgcca caattcatga 20

<210> 465
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
gtccttgcta tgggtctgaa ttatat 26

<210> 466
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466
actctctgca ccccacagtc accactatct c 31

<210> 467
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 467
ctgaggaacc agccatgtct ct 22

<210> 468
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
gaccagatgc aggtacagga tga 23

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<210> 469
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
ctgcccttc agtgatgcc aacctt 25

<210> 470
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 470
gggtggaggc tcaactgagta ga 22

<210> 471
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 471
caatacaggt aatgaaactc tgcttctt 28

<210> 472
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 472
tcctcttaag cataggccat ttctcagtt tagaca 36

<210> 473
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
ggtggtcttg cttggtctca c 21

<210> 474
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<220>
<223> Synthetic oligonucleotide probe

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<400> 474
ccgtcggttca gcaacatgac 20

<210> 475
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<220>
<223> Synthetic oligonucleotide probe

<400> 475
accgcctacc gctgtgccca 20

<210> 476
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
cagtaaaacc acaggctgga ttt 23

<210> 477
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 477
cctgagagca agaaggttga gaat 24

<210> 478
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
tagacaggga ccatggcccg ca 22

<210> 479
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
tgggctgtag aagagttggt g 21

<210> 480
<211> 20
<212> DNA
<213> Artificial Sequence

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 486
agcggcgctc ccagcctgaa t 21

<210> 487
<211> 23
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 487
catgattggt cctcagttcc atc 23

<210> 488
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 488
atagagggt cccagaagtg 20

<210> 489
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 489
cagggccttc aggccttca c 21

<210> 490
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 490
gctcagccaa acactgtoa 19

<210> 491
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 491
ggggccctga cagtgtt 17

Abstract

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<400> 492
ctgagccqag actgagcat ctacac 26
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<220>
<223> Synthetic oligonucleotide probe

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<210> 494
<211> 1231
<212> DNA
<213> Homo Sapien
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380

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 aagtgtctct ggcgtgtctga acggaggcaa atccatgagc cacaatgaat 1050
 caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100
 ccaggtgctg ttgaattctt ctgacagtcc ttcacccaaa agttcaaatt 1150
 tgtcagtgac atttaccaaa caaacaggca gagttcacta ttctatctgc 1200
 cattagacct tcttatcatc cataactaaag c 1231

<210> 495
 <211> 245
 <212> FRT
 <213> Homo Sapien

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 20 25 30
 Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val
 35 40 45
 Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg
 50 55 60
 Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser
 65 70 75
 Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp
 80 85 90
 Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile
 95 100 105
 Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys
 110 115 120
 Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu
 125 130 135
 Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn
 140 145 150
 Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
 155 160 165
 Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met
 170 175 180
 Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu
 185 190 195
 Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His
 200 205 210
 Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

0966037

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<210> 496
<211> 1471
<212> DNA
<213> Homo Sapien
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gacatggggg ggacttgggt aaaaaaggtat tatccagcca gagggctctgg 100
gagccctgtc ttaactgaacc tgggcaacct ggatattctg agacatatatt 150
tgggggggatt tcagtgaaaa aagtggggga tccctccat tttagagtga 200
gcaaaagaaa aaacaccaag gttgggttcc ttctctgacat tggcagtgcc 250
ccagtagggg tgggatgagc gaatattccc aaagctaaaag tcccacaccc 300
tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350
aaagtgccct gaagatatatt aaaccacgtc ttggaaattt agtgggtctt 400
ggctttggga tagtgtaagt gaggacagac actggagagg agggaaaggg 450
gacgttttca ataggaggca aaactcgagc gtgggatcca ctgaggagta 500
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cctgatccgg cagaagcggg aggtccgcga gcccgggggc agocggccgg 800
tgtcggcgca gcggcgctgt tgtcccogcg gcaccaagtc cctttgccag 850
aagcagctcc tcactcctgt gtccaagggt cgactgtgcg gggggcgccc 900
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aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000
atccagggca cccagagga taccagctcc ttacaccact tcaacctgat 1050
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acatggccat gaatgctgag ggactgctct acagttcgcc gcatcttaca 1150
gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtctctga 1200
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<212> DNA
<213> Homo Sapien

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gcaagaaccg cgggctctgc aacggcaacc tggtaggatat cttctccaaa 150
gtgcgcattc tcggcctcaa gaagcgcgagg ttgcggcgcc aagatcccca 200
gctcaagggt atagtaccca gggttatatt caggcaaggc tactacttgc 250
aaatgcaccc ogatggagct ctcgatggaa ccaaggatga cagcactaat 300
tctacactct toaacctcat accagtggga ctacgtgttg ttgccatcca 350
gggagtgtaaa acagggttgt atatagccat gaatggagaa gggtacctct 400
acccatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450
gaaaattatt atgtaatacta ctcatccatg ttgtacagac aacaggaaac 500
tggtagagcc tgggtttttg gattaaataa ggaaggcgaa gctatgaaag 550
ggaacagagt aaagaaaacc aaaccagcag ctcatcttct acccaagcca 600
ttggaagtgt ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650
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taatgaatgg aggcaaaacca gtcaacaaga gtaagacaac atag 744

<210> 499
<211> 247
<212> PRT
<213> Homo Sapien

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Ala Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg 30
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Ser Ser Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val 45
35 40 45
Asp Ile Phe Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg 60
50 55 60
Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu 75
65 70 75
Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala 90
80 85 90
Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn 105
95 100 105
Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys 120
110 115 120

Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro
 125 130 135
 Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe
 140 145 150
 Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln
 155 160 165
 Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln
 170 175 180
 Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His
 185 190 195
 Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser
 200 205 210
 Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro
 215 220 225
 Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro
 230 235 240
 Val Asn Lys Ser Lys Thr Thr
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<210> 500
 <211> 2906
 <212> DNA
 <213> Homo Sapien

<400> 500
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 caaaaa 2906

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 <211> 640
 <212> PRT
 <213> Homo Sapien

<400> 501
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 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
 35 40 45
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
 50 55 60
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
 65 70 75
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
 80 85 90
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
 95 100 105
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
 110 115 120
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
 125 130 135
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
 140 145 150
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
 155 160 165

Tyr	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu	Ile	Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325	Cys	Cys	Ala	Arg	Cys 330
Asn	Thr	Pro	Pro	Asn 335	Leu	Lys	Gly	Arg	Tyr 340	Ile	Gly	Glu	Leu	Asp 345
Gln	Asn	Tyr	Phe	Thr 350	Cys	Tyr	Ala	Pro	Val 355	Ile	Val	Glu	Pro	Pro 360
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Arg	Ala	Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
Gly	Thr	Val	Met	Thr 395	His	Gly	Ala	Tyr	Lys 400	Val	Arg	Ile	Ala	Val 405
Leu	Ser	Asp	Gly	Thr 410	Leu	Asn	Phe	Thr	Asn 415	Val	Thr	Val	Gln	Asp 420
Thr	Gly	Met	Tyr	Thr 425	Cys	Met	Val	Ser	Asn 430	Ser	Val	Gly	Asn	Thr 435
Thr	Ala	Ser	Ala	Thr 440	Leu	Asn	Val	Thr	Ala 445	Ala	Thr	Thr	Thr	Pro 450
Phe	Ser	Tyr	Phe	Ser 455	Thr	Val	Thr	Val	Glu 460	Thr	Met	Glu	Pro	Ser 465
Gln	Asp	Glu	Ala	Arg 470	Thr	Thr	Asp	Asn	Asn 475	Val	Gly	Pro	Thr	Pro 480

Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495

Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510

Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525

Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540

Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555

Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570

Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585

Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600

Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

<210> 502

<211> 2458

<212> DNA

<213> Homo Sapien

<400> 502

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agcaactgag cggggaagcg cccgcgtccg gggactggga tgtccctcct 200

ccttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

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<210> 503
 <211> 373
 <212> PRT
 <213> Homo Sapien

<400> 503
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 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro
 170 175 180
 Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu
 185 190 195
 Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala
 200 205 210
 Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val
 215 220 225

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Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
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 Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu
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 260 265 270
 Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
 275 280 285
 Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
 290 295 300
 Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
 305 310 315
 Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
 320 325 330
 Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
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<210> 504
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 <212> DNA
 <213> Homo Sapien

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<211> 352

<212> PRT

<213> Homo Sapien

<400> 505

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Lys	Ala	Lys	Gly	Glu	Thr	Ala	Tyr	Leu	Pro	Cys	Lys	Phe	Thr
			35						40				45
Ser	Pro	Glu	Asp	Gln	Gly	Pro	Leu	Asp	Ile	Glu	Trp	Leu	Ile
			50						55				60
Pro	Ala	Asp	Asn	Gln	Lys	Val	Asp	Gln	Val	Ile	Ile	Leu	Tyr
			65						70				75
Gly	Asp	Lys	Ile	Tyr	Asp	Asp	Tyr	Tyr	Pro	Asp	Leu	Lys	Gly
			80						85				90
Val	His	Phe	Thr	Ser	Asn	Asp	Leu	Lys	Ser	Gly	Asp	Ala	Ser
			95						100				105
Asn	Val	Thr	Asn	Leu	Gln	Leu	Ser	Asp	Ile	Gly	Thr	Tyr	Gln
			110						115				120
Lys	Val	Lys	Lys	Ala	Pro	Gly	Val	Ala	Asn	Lys	Lys	Ile	His

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Val Val Leu Val	Lys Pro Ser Gly Ala	Arg Cys Tyr Val	Asp Gly		
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Ser Glu Glu Ile	Gly Ser Asp Phe Lys	Ile Lys Cys Glu Pro	Lys		
	155	160	165		
Glu Gly Ser Leu	Pro Leu Gln Tyr Glu	Trp Gln Lys Leu Ser	Asp		
	170	175	180		
Ser Gln Lys Met	Pro Thr Ser Trp Leu	Ala Glu Met Thr Ser	Ser		
	185	190	195		
Val Ile Ser Val	Lys Asn Ala Ser Ser	Glu Tyr Ser Gly Thr	Tyr		
	200	205	210		
Ser Cys Thr Val	Arg Asn Arg Val Gly	Ser Asp Gln Cys Leu	Leu		
	215	220	225		
Arg Leu Asn Val	Val Pro Pro Ser Asn	Lys Ala Gly Leu Ile	Ala		
	230	235	240		
Gly Ala Ile Ile	Gly Thr Leu Leu Ala	Leu Ala Leu Ile Gly	Leu		
	245	250	255		
Ile Ile Phe Cys	Cys Arg Lys Lys Arg	Arg Glu Glu Lys Tyr	Glu		
	260	265	270		
Lys Glu Val His	His Asp Ile Arg Glu	Asp Val Pro Pro Pro	Lys		
	275	280	285		
Ser Arg Thr Ser	Thr Ala Arg Ser Tyr	Ile Gly Ser Asn His	Ser		
	290	295	300		
Ser Leu Gly Ser	Met Ser Pro Ser Asn	Met Glu Gly Tyr Ser	Lys		
	305	310	315		
Thr Gln Tyr Asn	Gln Val Pro Ser Glu	Asp Phe Glu Arg Thr	Pro		
	320	325	330		
Gln Ser Pro Thr	Leu Pro Pro Ala Lys	Phe Lys Tyr Pro Tyr	Lys		
	335	340	345		
Thr Asp Gly Ile	Thr Val Val				
	350				

<210> 506
 <211> 1705
 <212> DNA
 <213> Homo Sapien

<400> 506
 tgaaatgact tccacggctg ggacgggaac cttccacca cagctatgcc 50
 tctgattggt gaatggtgaa ggtgcctgtc taacttttct gtaaaaagaa 100
 ccagctgcct ccaggcagcc agccctcaag catcacttao aggaccagag 150
 ggacaagaca tgactgtgat gaggagctgc ttctgccaat ttaacaccaa 200
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

<213> Homo Sapien

<400> 507

Met	Asn	Phe	Gln	Gln	Arg	Leu	Gln	Ser	Leu	Trp	Thr	Leu	Ala	Arg	
1					5				10					15	
Pro	Phe	Cys	Pro	Pro	Leu	Leu	Ala	Thr	Ala	Ser	Gln	Met	Gln	Met	
			20						25					30	
Val	Val	Leu	Pro	Cys	Leu	Gly	Phe	Thr	Leu	Leu	Trp	Ser	Gln		
			35						40				45		
Val	Ser	Gly	Ala	Gln	Gly	Gln	Glu	Phe	His	Phe	Gly	Pro	Cys	Gln	
			50						55				60		
Val	Lys	Gly	Val	Val	Pro	Gln	Lys	Leu	Trp	Glu	Ala	Phe	Trp	Ala	
			65						70				75		
Val	Lys	Asp	Thr	Met	Gln	Ala	Gln	Asp	Asn	Ile	Thr	Ser	Ala	Arg	
			80						85				90		
Leu	Leu	Gln	Gln	Glu	Val	Leu	Gln	Asn	Val	Ser	Asp	Ala	Glu	Ser	
			95						100				105		
Cys	Tyr	Leu	Val	His	Thr	Leu	Leu	Glu	Phe	Tyr	Leu	Lys	Thr	Val	
			110						115				120		
Phe	Lys	Asn	His	His	Asn	Arg	Thr	Val	Glu	Val	Arg	Thr	Leu	Lys	
			125						130				135		
Ser	Phe	Ser	Thr	Leu	Ala	Asn	Asn	Phe	Val	Leu	Ile	Val	Ser	Gln	
			140						145				150		
Leu	Gln	Pro	Ser	Gln	Glu	Asn	Glu	Met	Phe	Ser	Ile	Arg	Asp	Ser	
			155						160				165		
Ala	His	Arg	Arg	Phe	Leu	Leu	Phe	Arg	Arg	Ala	Phe	Lys	Gln	Leu	
			170						175				180		
Asp	Val	Glu	Ala	Ala	Leu	Thr	Lys	Ala	Leu	Gly	Glu	Val	Asp	Ile	
			185						190				195		
Leu	Leu	Thr	Trp	Met	Gln	Lys	Phe	Tyr	Lys	Leu					
			200						205						

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

aaggagcagc cgcgaagcac caagtgaagt gcatgaagtt acagtgtgtt 50

tccctttggc tcctgggtac aatactgata ttgtgtctag tagacaacca 100

cgggtctcagg agatgtctga ttccacaga catgcacat atagaagaga 150

gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaaat 200

gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250

tgtgtgtctg gtagcaaga acctcctggc gttctacgtg gacagggtgt 300

tcaaggatca tcaggagcca aacccccaaa tcttgagaaa aatcagcagc 350
 attgccaaact ctttctctcta catgcagaaa actctgcggc aatgtcagga 400
 acagaggcag tgtcactgca ggcaggaagc caccaatgcc accagagtca 450
 tccatgacaa ctatgatcag ctggaggtcc acgctgctgc cattaaattcc 500
 ctgggagagc tcgaactctt tctagcctgg attaataaga atcatgaagt 550
 aatgtttctca gcttgatgac aaggaacctg tatagtgac cagggatgaa 600
 cccccctgt goggtttact gtgggagaca gccacacctg aaggggaagg 650
 agatggggaa gggcccttgc agctgaaagt cccactggct ggccctcaggc 700
 tgtcttattc cgcttgaaaa taggcaaaaa gtctactgtg gtatttgtaa 750
 taaactctat ctgctgaaag ggccctgcagg ccactcctgg agtaaagggc 800
 tgccttccca tctaatttat tgtaagtca tatagtccat gtctgtgatg 850
 tgagccaagt gatatcctgt agtacacatt gtactgagtg gtttttctga 900
 ataaattcca tattttacct atga 924

<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509

Met	Lys	Leu	Gln	Cys	Val	Ser	Leu	Trp	Leu	Leu	Gly	Thr	Ile	Leu	
1				5					10					15	
Ile	Leu	Cys	Ser	Val	Asp	Asn	His	Gly	Leu	Arg	Arg	Cys	Leu	Ile	
				20					25					30	
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys	
				35					40					45	
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu	
				50					55					60	
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys	
				65					70					75	
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe	
				80					85					90	
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser	
				95					100					105	
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln	
				110					115					120	
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn	
				125					130					135	
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His	
				140					145					150	
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala	

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
170 175

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<210> 510
<211> 996
<212> DNA
<213> Homo Sapien
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400> 510
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tggcttcggtt agaaccggcg tacaattaat acataacctt atgtatcata 100
cacatacgat ttaggtgaca ctatagaata acatccactt tgcctttctc 150
tccacagggtg tccactccca ggtccaactg caccctcggtt ctatcgataa 200
tctcagcacc agccactcag agcagggcac gatgttgggg gcccgccctca 250
ggctctgggt ctgtgccttg tgcagcgtct gcagcatgag cgctctcaga 300
gcctatccca atgcctcccc actgctcggc tccagctggg gtggcctgat 350
ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400
agaatggcca tgtggatggc gcaccccatc agaccatcta cagtgccttg 450
atgatcagat cagaggatgc tggctttgtg gtgattacag gtgtgatgag 500
cagaagatac ctctgcatgg atttcagagg caacattttt ggatcacact 550
atttcgaccg ggagaactgc aggttccaac accagacgct ggaaaacggg 600
tacgacgtct accactctcc tcagtatcac ttctgtgcta gtctgggccc 650
ggcgaagaga gccttctctg caggcatgaa cccacccccc tactcccagt 700
tcctgtcccc gaggaacgag atccccctaa ttcacttcaa cccccccata 750
ccacggcggc acacccggag cgccgaggac gactcggagc gggaccccct 800
gaacgtgctg aagccccggg cccgatgac cccggccccg gcctcctggt 850
cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaacca 900
ttaggggtgg tcaggggcgg tcgagtgaac acgcacgctg ggggaacggg 950
cccgaaagcc tgcccgccct tcgccaaagt catctagggt cgctgg 996

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<210> 511
<211> 251
<212> PRT
<213> Homo Sapien
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<400> 511
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser
1 5 10 15
Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
20 25 30

Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala
 35 40 45
 Thr Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His
 50 55 60
 Val Asp Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile
 65 70 75
 Arg Ser Glu Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser
 80 85 90
 Arg Arg Tyr Leu Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser
 95 100 105
 His Tyr Phe Asp Pro Glu Asn Cys Arg Phe Gln His Gln Thr Leu
 110 115 120
 Glu Asn Gly Tyr Asp Val Tyr His Ser Pro Gln Tyr His Phe Leu
 125 130 135
 Val Ser Leu Gly Arg Ala Lys Arg Ala Phe Leu Pro Gly Met Asn
 140 145 150
 Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg Arg Asn Glu Ile Pro
 155 160 165
 Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg His Thr Arg Ser
 170 175 180
 Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val Leu Lys Pro
 185 190 195
 Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln Glu Leu
 200 205 210
 Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu Gly
 215 220 225
 Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 230 235 240
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 245 250

<210> 512
 <211> 2015
 <212> DNA
 <213> Homo Sapien

<400> 512
 ggaaaaggta cccgcgagag acagccagca gttctgtgga gcagcgggtg 50
 cgggctagga tgggctgtct ctgggggtctg gctctgcccc ttttttcttt 100
 ctgctgggag gttgggggtct ctgggagctc tgcaggcccc agcaccgcga 150
 gaggagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200
 ctagaccgg gccacggcgc tctggaaact caaacgctga gcgctgagac 250
 ctcttttagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

ggggagccaa gagaatttcc cctgcaagag agaccaggag ttccacaaaa 350
 acatctccca acttcatggt gctgatcgcc acctccgttg agacatcagc 400
 cgccagtggc agccccgag gagetggaat gaccacagtt cagaccatca 450
 caggcagtga tcccaggga gccatctttg acaccctttg caccgatgac 500
 agctctgaag aggcaaagac actcacaatg gacatattga cattggctca 550
 caccctccca gaagctaagg gcctgtctc agagagcagt gcctcttccg 600
 acggccccc tccagtcac accccgtcac gggcctcaga gaggcgcgc 650
 tcttcgacg gcccccac agtcatcacc ccgtcacggg cctcagagag 700
 cagcgctct tccgacggc cccatccagt catcaccccg tcattggtcc 750
 cgggatctga tgtcactct ctcgctgaag ccttggtgac tgtcacaaa 800
 atcgaggtta ttaattgcag catcacagaa atagaaacaa caacttccag 850
 catccctggg gcctcagaca tagatctcat cccacaggaa ggggtgaagg 900
 cctcgtccac ctccgatcca ccagctctgc ctgactccac tgaagcaaaa 950
 ccacacatca ctgaggtcac agcctctgcc gagaccctgt ccacagcccg 1000
 caccacagag tcagctgcac ctcatgccac ggttgggacc ccactcccca 1050
 ctaacagcgc cacagaaaga gaagtgcag cacccgggc cagcaccctc 1100
 agtggagctc tggtcacagt tagcaggaat cccctggaag aaacctcagc 1150
 cctctctgtt gagacacaa gttacgtcaa agtctcagga gcagctccgg 1200
 tctccataga ggctgggtca gcagtgggca aaacaactc ctttctggg 1250
 agctctgctt cctctacag cccctggaa gcgcctca agaactcac 1300
 ccttcagag acaccgacca tggacatgc aaccaaggg cccttcccca 1350
 ccagcaggga cctcttctt tctgtccctc cgactacaac caacagcagc 1400
 cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450
 gatgaagccc caacagccc gccccagact gcccgagca ggcgagaccac 1500
 agacgtgagt gcaggtgaaa atggagggtt cctcctctg cggtctgagt 1550
 tggcttcccc ggaagacctc actgaccca gaggggcaga aaggctgatg 1600
 cagcagctcc accgggaact ccacgccac gcgcctcact tccaggtctc 1650
 cttaactcgt gtcaggagag gctaacggac atcagctgca gccaggcatg 1700
 tcccgatgc caaaagaggg tgctgccctt agcctgggc cccaccgaca 1750
 gactgcagct gcgttactgt gctgagaggt acccagaagg tccccatgaa 1800
 gggcagcatg tccaagcccc taaccocaga tgtggcaaca ggaccctcgc 1850
 tcacatccac cggagtgtat gtatggggag gggcttcacc tgttccaga 1900

gggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950
 acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcaactcagt 2000
 gtggcccaaa aaaaa 2015

<210> 513
 <211> 482
 <212> PRT
 <213> Homo Sapien

<400> 513
 Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys
 1 5 10 15
 Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg
 20 25 30
 Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
 35 40 45
 Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
 50 55 60
 Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
 65 70 75
 Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
 80 85 90
 Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
 95 100 105
 Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
 110 115 120
 Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
 125 130 135
 Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
 140 145 150
 Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
 155 160 165
 Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
 170 175 180
 Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
 185 190 195
 Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
 200 205 210
 Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
 215 220 225
 Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
 230 235 240
 Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
 245 250 255

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480
Gln Thr																	

<210> 514
 <211> 2284
 <212> DNA
 <213> Homo Sapien

<400> 514
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 tccttcccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100
 ggcgcggggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
 cttcttaaag caaactaaga ccagaggagg gattatcctt gacctttgaa 200
 gacccaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250

tgacttacac tttggttaata atttgcttcc tgacactaag gctgtctgct 300
 agtcagaatt gcctcaaaaa gagtctagaa gatgttgta ttgacatcca 350
 gtcattctctt tetaaggaa tcagaggcaa tgagcccgta tatacttcaa 400
 ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450
 gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
 acccaactgc taccattttt tctgtcccaa cgaggagacc tgtccattga 550
 aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
 ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650
 acatggccaa ttttcacaag cagtactctc cctagcccat catcacacag 700
 attattcaaa gccaccgat atctcatgga gagacacact ttctcagaag 750
 ttggatcct cagatcacct ggagaaacta tttaagatgg atgaagcaag 800
 tgccagctc cttgcttata agggaaaagg ccattctcag agttcacaa 850
 ttctcttga tcaagaaata gctcatctgc tgccgaaaaa tgtgagtgcg 900
 ctccagcta cgggtggcagt tgettctcca cataccacct cggctactcc 950
 aaagccgcc acccttctac ccaccaatgc ttcagtaca cttctggga 1000
 cttccagcc acagctggcc accacagctc cactgttaac cactgtcact 1050
 tctcagctc ccacgacct catttctaca gtttttacac gggctgcggc 1100
 taccctcaa gcaatggcta caacagcagt tctgactacc accttcagg 1150
 caccacgga ctcgaaaggc agcttagaaa ccataccgtt tacagaaac 1200
 tccaacttaa ctttgaacac agggaatgtg tataacccta ctgcacttc 1250
 tatgtcaaat gtggagctct ccactatgaa taaaactgct tcttgggaag 1300
 gtaggggagc cagtccaggc agttctctcc agggcagtgt tccagaaaa 1350
 cagtacggcc ttccatttga aaaatggctt cttatogggg cctgtctctt 1400
 tgggtgctcg ttctgggtga taggcctcgt cctcctgggt agaactcctt 1450
 cggaatcact ccgaggaaa cgttaactca gactggatta ttgatcaat 1500
 gggatctatg tggacatcta aggatggaac tgggtgtctc ttaattcatt 1550
 tagtaaccag aagcccaaat gcaatgagtt tctgtcgact tgctagtctt 1600
 agcaggagggt tgatatttga agacaggaaa atgccccctt ctgctttcct 1650
 tttttttttt ggagacagag tcttgctctg ttgccaggc tggagtgcag 1700
 tagcacgac tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750
 ttctctgccc tcagctctc aagtatctgg gattacaggc atgtgccacc 1800
 acacctgggt gatattttag ttttagtag agacgggggt tcaccatgtt 1850

09573 103

<400> 515

Met	Phe	Phe	Gly	Gly	Glu	Gly	Ser	Leu	Thr	Tyr	Thr	Leu	Val	Ile
1				5					10					15
Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu
				20					25					30
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu
				35					40					45
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln
				50					55					60
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly
				65					70					75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala
				80					85					90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala
				95					100					105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile
				110					115					120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu
				125					130					135
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val
				140					145					150
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp
				155					160					165
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp
				170					175					180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu
				185					190					195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
 200 205 210
 Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
 215 220 225
 Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
 230 235 240
 Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
 245 250 255
 Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
 260 265 270
 Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
 275 280 285
 Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
 290 295 300
 Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly
 305 310 315
 Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
 320 325 330
 Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
 335 340 345
 Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
 350 355 360
 Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
 365 370 375
 Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
 380 385 390
 Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
 395 400 405
 Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
 410 415 420
 Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
 425 430

<210> 516
 <211> 2749
 <212> DNA
 <213> Homo Sapien

<220>
 <221> unsure
 <222> 1869, 1887
 <223> unknown base

<400> 516
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 ttgctgtcgt ctcccagggt atgaagccct ggagggccca gaggaatca 100

gcggttcga aggggacact gtgtccctgc agtgaccta caggaagag 150
 ctgagggacc accggaagta ctggtgcagg aagggtgga tctcttctc 200
 tcgctgtctt ggcacatct atgcagaaga agaaggccag gagacaatga 250
 agggcagggt gtccatccgt gacagccgc aggagctctc gctcattgtg 300
 acctgtgga acctaccct gcaagacgct gggagtagt ggtgtgggtg 350
 cgaaaaacgg ggcgccgatg agtctttact gatctctctg ttctctttc 400
 caggaccctg ctgtctctcc tcccttctc ccaccttcca gcctctggct 450
 acaacacgcc tgcagcccaa ggcaaaagct cagcaaaccc agccccagg 500
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Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr
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Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile
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Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser
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Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala
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Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu
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Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu
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Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr
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Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro
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Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala
215 220 225

Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg
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Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu
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Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys
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